

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 20:03:45 ; Search time 12448.6 Seconds

(without alignments)
13249.270 Million cell updates/sec

Title: US-09-993-420A-1

Perfect score: 6560
Sequence: 1 atcgatagtcgtcaccaaat.....gttgtataaaattatcaaa 6560

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	6541.8	99.7	6560	US-09-993-420A-1	Sequence 1, Appl1
2	6529.8	99.5	6559	US-07-927-681-1	Sequence 1, Appl1
3	6529.8	99.5	6559	US-08-288-295-1	Sequence 1, Appl1
4	6529.8	99.5	6559	US-08-801-248-1	Sequence 1, Appl1
5	713	10.9	713	US-60-360-039-19563	Sequence 29563, A
6	632.6	9.6	1315	US-07-927-681-2	Sequence 2, Appl1
7	632.6	9.6	1315	US-08-288-295-2	Sequence 2, Appl1
8	632.6	9.6	1315	US-08-288-295-4	Sequence 4, Appl1
9	632.6	9.6	1315	US-08-288-295-5	Sequence 4, Appl1
10	632.6	9.6	1315	US-08-801-248-2	Sequence 6, Appl1
11	632.6	9.6	1315	US-08-801-248-5	Sequence 2, Appl1
12	632.6	9.6	1315	US-08-801-248-6	Sequence 4, Appl1
13	632.6	9.6	1315	US-09-993-420A-2	Sequence 5, Appl1
14	632.6	9.6	1315	US-09-993-420A-4	Sequence 6, Appl1
15	632.6	9.6	1315	US-09-993-420A-5	Sequence 4, Appl1
16	632.6	9.6	1315	US-09-993-420A-6	Sequence 5, Appl1
17	632.6	9.6	1315	US-09-993-420A-6	Sequence 6, Appl1
18	632.6	9.6	1315	US-09-993-420A-6	Sequence 5, Appl1
19	149	2.3	716	US-60-360-039-29178	Sequence 29178, A
20	139.2	2.1	7653	US-07-979-658-18	Sequence 18, Appl1
21	139.2	2.1	7653	US-07-984-182-1	Sequence 1, Appl1

C	22	139.2	2.1	7653	4	US-08-080-850A-1	Sequence 1, Appl1
C	23	139.2	2.1	7653	6	US-08-258-287A-1	Sequence 1, Appl1
C	24	139.2	2.1	7653	6	US-08-282-211-1	Sequence 1, Appl1
C	25	139.2	2.1	7653	6	US-08-282-211A-1	Sequence 1, Appl1
C	26	139.2	2.1	7653	6	US-08-287-669-18	Sequence 18, Appl1
C	27	139.2	2.1	7653	7	US-08-368-704A-1	Sequence 1, Appl1
C	28	139.2	2.1	7653	7	US-08-368-704B-1	Sequence 1, Appl1
C	29	139.2	2.1	7653	7	US-08-394-189-1	Sequence 1, Appl1
C	30	139.2	2.1	7653	8	US-08-459-455-1	Sequence 1, Appl1
C	31	139.2	2.1	7653	13	US-08-854-763-1	Sequence 1, Appl1
C	32	139.2	2.1	7653	14	US-09-083-662-1	Sequence 1, Appl1
C	33	139.2	2.1	7653	21	US-09-549-066-1	Sequence 1, Appl1
C	34	139.2	2.1	7653	22	US-09-577-897-18	Sequence 18, Appl1
C	35	139.2	2.1	7653	33	US-09-888-243-1	Sequence 1, Appl1
C	36	122.8	1.9	6559	7	US-07-927-681-1	Sequence 1, Appl1
C	37	122.8	1.9	6559	6	US-08-288-295-1	Sequence 1, Appl1
C	38	122.8	1.9	6559	12	US-08-801-248-1	Sequence 1, Appl1
C	39	122.8	1.9	6560	37	US-09-993-420A-1	Sequence 1, Appl1
C	40	121.4	1.9	716	80	US-06-360-039-29178	Sequence 29178, A
C	41	121	1.8	42521	1	PCT-US00-14462A-23	Sequence 23, Appl1
C	42	121	1.8	42521	1	PCT-US99-01313-23	Sequence 23, Appl1
C	43	121	1.8	42521	16	US-09-235-810-23	Sequence 23, Appl1
C	44	121	1.8	42521	17	US-09-373-658-23	Sequence 23, Appl1
C	45	121	1.8	42521	17	US-09-373-658B-23	Sequence 23, Appl1

ALIGNMENTS

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RESULT 1
US-09-993-420A-1
: Sequence 1, Application US/09993420A
:
: GENERAL INFORMATION:
:
: APPLICANT: Horvitz, H. Robert
: APPLICANT: Hengartner, Michael
: TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
: TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: 01997/201006
: CURRENT APPLICATION NUMBER: US/09/993,420A
: CURRENT FILING DATE: 5001-11-09
: PRIOR APPLICATION NUMBER: 09/234,186
: PRIOR FILING DATE: 1999-01-20
: PRIOR APPLICATION NUMBER: 07/898,933
: PRIOR FILING DATE: 1992-06-12
: PRIOR APPLICATION NUMBER: 07/927,681
: PRIOR FILING DATE: 1992-08-10
: PRIOR APPLICATION NUMBER: 08/288,295
: PRIOR FILING DATE: 1994-08-10
: PRIOR APPLICATION NUMBER: 08/801,248
: PRIOR FILING DATE: 1997-02-19
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 6560
: TYPE: DNA
: ORGANISM: Caenorhabditis elegans
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(6559)
: OTHER INFORMATION: n = A,T,C OR G
US-09-993-420A-1

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Query Match	99.78;	Score 6541.8;	DB 37;	Length 6560;
Best Local Similarity	100.08;	Pred. No. 0;		
Matches 6560;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db 1 ATCGATTCTGCGCAACCAATGGATTTCGCCATTTCTACATGTGTCATAGGGCTCAACAATTTA 60

Qy 61 CAAATCTCGAGAAAAGCAAGATGCCAAGGAGTATGAAGAGTTCGCAATCTTAATATTT 120

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Db	121	TAATTTAAAAAATCAATTTGCAATTTGAATTTCAACTCTACTCTGTTTGAATAATCCGA	180
Qy	181	TTCCTTTAAAGAAACCTCTGGATCGCCCATTTCTTCTCCAGAAATTCCTTCAAGTAGTGTT	240
Db	181	TTCCTTTAAAGAAACCTCTGGATCGCCCATTTCTTCTCCAGAAATTCCTTCAAGTAGTGTT	240
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Db	241	TTGTACTGATTTTCTCCGCAAAAGATAGGAACCTTCGATCTCTGAGCGAAACGGAT	300
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Qy	481	GGATACAAATTTGSAGAAATTTAGATTTCATCTTGAATTTGCAAATGGAAAAATATTT	540
Db	481	GGATACAAATTTGSAGAAATTTAGATTTCATCTTGAATTTGCAAATGGAAAAATATTT	540
Qy	541	ATTCAAGAAATTCACAGAAAAATGCACAAAAAACAACAAAAAGAACAAAAACAAGTC	600
Db	541	ATTCAAGAAATTCACAGAAAAATGCACAAAAAACAACAAAAAGAACAAAAACAAGTC	600
Qy	601	GAAAGTGGCCCGGGGCTGTGTGAGAGCATCTTCTTAAACGAGAGCGCGTGTGGCGC	660
Db	601	GAAAGTGGCCCGGGGCTGTGTGAGAGCATCTTCTTAAACGAGAGCGCGTGTGGCGC	660
Qy	661	ACTTCTGTGCGCCCTGTGCGATTCCTCCGCAAAAAATTCACAACTGTGTTTGAACGCA	720
Db	661	ACTTCTGTGCGCCCTGTGCGATTCCTCCGCAAAAAATTCACAACTGTGTTTGAACGCA	720
Qy	721	CCGCCCTGTTCTTTTTCATTTTGTATPAGAAATTCAGATTTGAGATATATTAAC	780
Db	721	CCGCCCTGTTCTTTTTCATTTTGTATPAGAAATTCAGATTTGAGATATATTAAC	780
Qy	781	ATTCCAACTGCGATTTGTGTCCCGCTTGGGCGCGACAGATGCTGATTTCCGCTCTTTGGA	840
Db	781	ATTCCAACTGCGATTTGTGTCCCGCTTGGGCGCGACAGATGCTGATTTCCGCTCTTTGGA	840
Qy	841	ACATGATGCTCACCAAGTGGGGATTTTTCATTTTCCGTGAAATTTGTATTTTT	900
Db	841	ACATGATGCTCACCAAGTGGGGATTTTTCATTTTCCGTGAAATTTGTATTTTT	900
Qy	901	TTGTGACGATGAGAGGAATGTATPACAGACACATTCCTTTCAATTAATTAATTTAA	960
Db	901	TTGTGACGATGAGAGGAATGTATPACAGACACATTCCTTTCAATTAATTAATTTAA	960
Qy	961	TATTCACAGTCCGAGGCAAGAGCCCAATTCAGAGTTCGGATTTAGCTGTGAAG	1020
Db	961	TATTCACAGTCCGAGGCAAGAGCCCAATTCAGAGTTCGGATTTAGCTGTGAAG	1020
Qy	1021	CAGGCTCACAAGATTCGCCCAATTCGCTCCCATCTCACGATCTACAGCACAATTTGACC	1080
Db	1021	CAGGCTCACAAGATTCGCCCAATTCGCTCCCATCTCACGATCTACAGCACAATTTGACC	1080
Qy	1081	TGGATGCTCTCCGGATTCATAGAAATCAGCGTGTGTATGTGCGGAAACCTCTCGTC	1140
Db	1081	TGGATGCTCTCCGGATTCATAGAAATCAGCGTGTGTATGTGCGGAAACCTCTCGTC	1140
Qy	1141	GGAGAAATTCGATTCGCAAGTTTGGCGCTTCGATTTACGCGTTTGTGATTTCAATCCGT	1200
Db	1141	GGAGAAATTCGATTCGCAAGTTTGGCGCTTCGATTTACGCGTTTGTGATTTCAATCCGT	1200

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Db	1201	ACCTGGAACTTACATGCGCGGTGACCCCTGTCCTCAAGTACATCATGCTTTCCCATC	1260
QY	1261	ATTTCACATACCTTACGCGAATTCGCTCTTAGATTCGATTTGGCTAAGGAGTCAAT	1320
Db	1261	ATTTCACATACCTTACGCGAATTCGCTCTTAGATTCGATTTGGCTAAGGAGTCAAT	1320
QY	1321	AATGTTGACAGGTAGAGTGAATAATTAATTAATTTGTTTTAAATAAATAATTAAT	1380
Db	1321	AATGTTGACAGGTAGAGTGAATAATTAATTAATTTGTTTTAAATAAATAATTAAT	1380
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Db	1381	TTTCACATCTACAAATCGGGATATCTCGTATCTGGAAGCTTGGCGTATCTGCTGCCA	1440
QY	1441	TTGCTTCAACTCTTGGCAGAAACAGACACAGACTGCTAGGACAGATGCTCGGCC	1500
Db	1441	TTGCTTCAACTCTTGGCAGAAACAGACACAGACTGCTAGGACAGATGCTCGGCC	1500
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Db	1621	GCTAGAAATGATATATATGATTAATGAAGAAACGAATAAAAATTTAGATGACACGCTGCAG	1680
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QY	1801	CAGGACTTCCCATCACCAGTAGGACAGGCTTCGACGCGAAGAAATGTCATCGGAGACTCA	1860
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Db	2041	CAACCGGACGCAAAATGATGCGAGTATGGGAAACGATATTCAGAGAAAGACACGGGAA	2100
QY	2101	AATTTTGAAGACCTTCTGTGAGACACTGCTCGAGTGGCCAGAAATCTCATTTACTGTAT	2160
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Db	2161	CAGGATGTGTTTGGAGGTTTGGAAATGACACAGACAGATCAATGTCTTATGGA	2220
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QY	2281	AGGTGGCAGAAAAAATCATTTGCAAAAAATGTTTGTCTTCTCAGGAATACGAAAACT	2340
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QY	2521	GGCAAAAAGATCGTGTGATTTTCAAAAAATCGGTTTTTAATGTATAATTTGTGAAAAAT	2580
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QY	2581	ACATTTAAATTCGATTTTGAACCTTTTCTCGAAAAACAGGTTTTTCTGCTGATTTGC	2640
Db	2581	ACATTTAAATTCGATTTTGAACCTTTTCTCGAAAAACAGGTTTTTCTGCTGATTTGC	2640
QY	2641	TGAGCAAAAACCCCAAAATTCATTTTCGACATTTAAAAACAGAAAAATCGTTTTTT	2700
Db	2641	TGAGCAAAAACCCCAAAATTCATTTTCGACATTTAAAAACAGAAAAATCGTTTTTT	2700
QY	2701	TAAAGTTAATTTCCGCGCAAAATGAGAAATTAATTTGCAAAATTTCTAATTTCAAGTA	2760
Db	2701	TAAAGTTAATTTCCGCGCAAAATGAGAAATTAATTTGCAAAATTTCTAATTTCAAGTA	2760
QY	2761	GCTCTAATCTCGTTGCGCGGTTTCGTAGCTGCAGAAAAATGAGAGGATCGTGAAGTCTCAG	2820
Db	2761	GCTCTAATCTCGTTGCGCGGTTTCGTAGCTGCAGAAAAATGAGAGGATCGTGAAGTCTCAG	2820
QY	2821	GGACAAGTCCGAAACCTCTCTGTTTACACATTCGCTTATCAAAACCGGATCCGAC	2880
Db	2821	GGACAAGTCCGAAACCTCTGTTTACACATTCGCTTATCAAAACCGGATCCGAC	2880
QY	2881	AACTGGAAGGAACACAAATCGAGCTGGGTAAAGAGATTTTCTATAGACATTAAGAACAA	2940
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QY	2941	TATCCCTTTTCCCTTAAGTACCTCTGACTTCCCGGGGTGTGTGAAGCCGATTAATTCAGG	3000
Db	2941	TATCCCTTTTCCCTTAAGTACCTCTGACTTCCCGGGGTGTGTGAAGCCGATTAATTCAGG	3000
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Db	3001	GTTGGTATGCTCTTGGGGGGACACCTGGAAGAAATTCAGTATTTACTGTTTATGAT	3060
QY	3061	AATGTTATTTGTTACGGAATACAAAAATTCGAGAAATGCTATTTCAACAATATTTGACGC	3120
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4261 GCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4320
4261 GCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4320
4321 GTATATTAACAAAAAGCTAGTACGATTCAAAAAAGCAATTTGCTTACTAT 4380
4321 GTATATTAACAAAAAGCTAGTACGATTCAAAAAAGCAATTTGCTTACTAT 4380
4381 TCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4440
4381 TCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4440
4441 TCAAGGCTACAACTATTTGTAATTAAGAGATTCAGAGGATTTACCTTTGGAGAA 4500
4441 TCAAGGCTACAACTATTTGTAATTAAGAGATTCAGAGGATTTACCTTTGGAGAA 4500

4441 TCAAGGCTACAACTATTTGTAATTAAGAGATTCAGAGGATTTACCTTTGGAGAA 4500
4501 AGATACCTGAGATTTTCACTTTGCTTACCTGAAACGGCTTAAAAAGCTAAAAAG 4560
4501 AGATACCTGAGATTTTCACTTTGCTTACCTGAAACGGCTTAAAAAGCTAAAAAG 4560
4561 CTTAAAAATGAGTTTTCACCTGTTTTCAAAAAAGCAAGCTTACAGCTTTTAC 4620
4561 CTTAAAAATGAGTTTTCACCTGTTTTCAAAAAAGCAAGCTTACAGCTTTTAC 4620
4621 GAGATTTTCAATTAATTTGATTTGAAATTTTCAATTTTCAATTTTCAATTTTCA 4680
4621 GAGATTTTCAATTAATTTGATTTGAAATTTTCAATTTTCAATTTTCAATTTTCA 4680
4681 GAAATTTTGGATTTTGAAGCTTAAATAGATTCCTGCTGCTGCTGCTGCTGCTGCT 4740
4681 GAAATTTTGGATTTTGAAGCTTAAATAGATTCCTGCTGCTGCTGCTGCTGCTGCT 4740
4741 TTAATTTCAAAAAAGATGCTGCTTAAAGAGTCTGATTTGAAACTTCTGTTTGC 4800
4741 TTAATTTCAAAAAAGATGCTGCTTAAAGAGTCTGATTTGAAACTTCTGTTTGC 4800
4801 GCACTTTTCACTGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4860
4801 GCACTTTTCACTGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4860
4861 AAATTTAATTTTACCGATCGCAAAAAAAGAAAGCAAGCAAGCAAGCAAGCAAGCA 4920
4861 AAATTTAATTTTACCGATCGCAAAAAAAGAAAGCAAGCAAGCAAGCAAGCAAGCA 4920
4921 CAACAATGATTTGAATTTACGATCTTTTAAAGGNNCAATTTCTGATTTTACAC 4980
4921 CAACAATGATTTGAATTTACGATCTTTTAAAGGNNCAATTTCTGATTTTACAC 4980
4981 AAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5040
4981 AAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5040
5041 AATGTTTCAAAAAAAGCAATTTGAGCAATTTGAGCTTAAAGCAAGCAAGCAAGCA 5100
5041 AATGTTTCAAAAAAAGCAATTTGAGCAATTTGAGCTTAAAGCAAGCAAGCAAGCA 5100
5101 TCTAAAAATTAATAAATATTCGAAATTTGATTTGATTTGATTTGATTTGATTTGAT 5160
5101 TCTAAAAATTAATAAATATTCGAAATTTGATTTGATTTGATTTGATTTGATTTGAT 5160
5161 AATGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5220
5161 AATGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5220
5221 AAAGCAGANNACGATTTTTCGCAATTTTTCCTGACGCTGCAATTTTGAACCTC 5280
5221 AAAGCAGANNACGATTTTTCGCAATTTTTCCTGACGCTGCAATTTTGAACCTC 5280
5281 TAAATAGCTGATTTTTCCTGATTTGCAATTTTTCCTGATTTTTCCTGATTTTTCCT 5340
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5341 TATTTAGCTGATTTTTCCTGATTTGCAATTTTTCCTGATTTTTCCTGATTTTTCCT 5400
5341 TATTTAGCTGATTTTTCCTGATTTGCAATTTTTCCTGATTTTTCCTGATTTTTCCT 5400
5401 TATTTAGCTGATTTTTCCTGATTTGCAATTTTTCCTGATTTTTCCTGATTTTTCCT 5460
5401 TATTTAGCTGATTTTTCCTGATTTGCAATTTTTCCTGATTTTTCCTGATTTTTCCT 5460
5461 TATTTAGCTGATTTTTCCTGATTTGCAATTTTTCCTGATTTTTCCTGATTTTTCCT 5520
5461 TATTTAGCTGATTTTTCCTGATTTGCAATTTTTCCTGATTTTTCCTGATTTTTCCT 5520
5521 TGCATGCAACAAAGAGAGTCTGATTTTTCCTGATTTTTCCTGATTTTTCCTGATTT 5580
5521 TGCATGCAACAAAGAGAGTCTGATTTTTCCTGATTTTTCCTGATTTTTCCTGATTT 5580
5581 TGCATGCAACAAAGAGAGTCTGATTTTTCCTGATTTTTCCTGATTTTTCCTGATTT 5640
5581 TGCATGCAACAAAGAGAGTCTGATTTTTCCTGATTTTTCCTGATTTTTCCTGATTT 5640

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Db 421 AGGATAAAGGCTCATTTTGAAGCCGAATTTACTAAATCTCTAGCCATGAGCGAT 480
OY 481 GGATCGAAATTCGAGAAATTTAGATTCATCTGAAATTCGAATGGAATAAT 540
Db 481 GGATCGAAATTCGAGAAATTTAGATTTATCTTGAATTTGCAATGGAATAAT 540
OY 541 ATTCAAGAAATACAGAAATGCAACAAACAAAAAGAAAAAGAAAAAGAAACAAATGTC 600
Db 541 ATTCAAGAAATACAGAAATGCAACAAACAAAAAGAAAAAGAAAAAGAAACAAATGTC 600
OY 601 GAAAGTGGCCCCGGGCTTTTCTGACGATCTCTCAAGAGAGAGCGCTGGTGGCG 660
Db 601 GAAAGTGGCCCCGGGCTTTTCTGACGATCTCTCAAGAGAGAGCGCTGGTGGCG- 659
OY 661 ACTTCTGTCCTGTCGTCGATTTTCGCAACAAATTCACACTTTTGAAGCA 720
Db 660 ACTTCTGTCCTGTCGTCGATTTTCGCAACAAATTCACACTTTTGAAGCA 719
OY 721 CCGCCCTGTTCTTTTCAATTTGATTAAGAAATCAGCATTTCTCAGATGATTAAC 780
Db 720 CCGCCCTGTTCTTTTCAATTTGATTAAGAAATCAGCATTTCTCAGATGATTAAC 779
OY 781 ATTCCAACTGATTCGTGCGCTTGCGCCGATCGATTCGATTCGCGCTCTTGA 840
Db 780 ATTCCAACTGATTCGTGCGCTTGCGCCGATCGATTCGATTCGCGCTCTTGA 839
OY 841 ACATGATCGTCACCAAGTGGGATTTTGAATTTTCCGTAATAATGTTGATTTT 900
Db 840 ACATGATCGTCACCAAGTGGGATTTTGAATTTTCCGTAATAATGTTGATTTT 899
OY 901 TGTGTACGATGAAGAGAAATGTTATAACACACATCTCTTCAATTAATTAATA 960
Db 900 TGTGTACGATGAAGAGAAATGTTATAACACACATCTCTTCAATTAATTAATA 959
OY 961 TATTCACAGTCGAGGCAAGACCAATCAGAAATTCGATGGGATTAACCTGTTGAG 1020
Db 960 TATTCACAGTCGAGGCAAGACCAATCAGAAATTCGATGGGATTAACCTGTTGAG 1019
OY 1021 CAGCGCTCCAGAAATCGCCCATGCTCACATCTCACCCTGTACACGCAATGAGC 1080
Db 1020 CAGCGCTCCAGAAATCGCCCATGCTCACATCTCACCCTGTACACGCAATGAGC 1079
OY 1081 TGGATGCTCTCGGATTCATAGAAATCAGCGTGTGTAATGCGGAAACCTTCTGCTC 1140
Db 1080 TGGATGCTCTCGGATTCATAGAAATCAGCGTGTGTAATGCGGAAACCTTCTGCTC 1139
OY 1141 GGAGGAATCGAATTCGAGTTTGGCGTTTCGATTCACCGCTTTTGTGATTTCACTCGT 1200
Db 1140 GGAGGAATCGAATTCGAGTTTGGCGTTTCGATTCACCGCTTTTGTGATTTCACTCGT 1199
OY 1201 AGCTGGAATTCATTCATGCGCGGTGACCGCTGTCTCAAGTACATGCTTCCCATC 1260
Db 1200 AGCTGGAATTCATTCATGCGCGGTGACCGCTGTCTCAAGTACATGCTTCCCATC 1259
OY 1261 ATTTCCATCTCTTAAGGAAATTCGTTCTTAGAATTCGATTTGGCTAAGGAGTCAAT 1320
Db 1260 ATTTCCATCTCTTAAGGAAATTCGTTCTTAGAATTCGATTTGGCTAAGGAGTCAAT 1319
OY 1321 AATGTTGACAGGTAGAGTTGAATTAATTAATTAATTTAAATTAATTAAT 1380
Db 1320 AATGTTGACAGGTAGAGTTGAATTAATTAATTAATTTAAATTAATTAAT 1379
OY 1381 TTCAATCTACAAATCGGATTCCTGATTCGACTTTCGCTATCTCTGCTCGCA 1440
Db 1380 TTCAATCTACAAATCGGATTCCTGATTCGACTTTCGCTATCTCTGCTCGCA 1439
OY 1441 TTGCTTCACTCTTGGCAGAACAGACAGACAGCTGCTAGGACAGATCTCCGC 1500
Db 1440 TTGCTTCACTCTTGGCAGAACAGACAGACAGCTGCTAGGACAGATCTCCGC 1499
OY 1501 TTCTTTTCTTACTCGCCGACGCTTCGACATTTCTGTAATTTACTTTTACCGTTG 1560
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Db 1500 TTCTTTTCTTACTCGCCGACCCCTCGACATTTCTGTAATTTACTTTTACCGTTG 1559
OY 1561 ATTTCTTCGATTTTCTCTCTTTTCCGTAGATTTTACTCTCTCTCTCTCTCTCT 1620
Db 1560 ATTTCTTCGATTTTCTCTCTTTTCCGTAGATTTTACTCTCTCTCTCTCTCTCT 1619
OY 1621 GTCTAGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1680
Db 1620 GTCTAGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1679
OY 1681 GCGGACAACTGCTGACGAATTCGCGCTATCGCGACGAAACGATGGGATGCGAGATG 1740
Db 1680 GCGGACAACTGCTGACGAATTCGCGCTATCGCGACGAAACGATGGGATGCGAGATG 1739
OY 1741 AAGGATTCCTGGGATTAAGGACAGACGACCCGATTTTGAATTAATGATGATGCT 1800
Db 1740 AAGGATTCCTGGGATTAAGGACAGACGACCCGATTTTGAATTAATGATGATGCT 1799
OY 1801 CAGGATTCGCTATCCAGATGAGCAGGCTTCGACGCGGAAGATGTCATCGAGATCA 1860
Db 1800 CAGGATTCGCTATCCAGATGAGCAGGCTTCGACGCGGAAGATGTCATCGAGATCA 1859
OY 1861 ATTGATGAAATTCATGATTTGGGAGAGCCAGGCTGATTCGAGGATTTGTGTA 1920
Db 1860 ATTGATGAAATTCATGATTTGGGAGAGCCAGGCTGATTCGAGGATTTGTGTA 1919
OY 1921 ATTTTAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1980
Db 1920 ATTTTAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1979
OY 1981 CACCGAATCCGCAAAACGGAATGATGTTGAGACACCGGATTCCTGTGAGATG 2040
Db 1980 CACCGAATCCGCAAAACGGAATGATGTTGAGACACCGGATTCCTGTGAGATG 2039
OY 2041 CAACCGGACGCAAGAAATGATGAGTATGGAACGATTCGAGAAACAGCAGCGAA 2100
Db 2040 CAACCGGACGCAAGAAATGATGAGTATGGAACGATTCGAGAAACAGCAGCGAA 2099
OY 2101 AATTTGAGACTCTCTGACAGCTGCTGCAAGTCCGCAATCTCATTTTCACTGAT 2160
Db 2100 AATTTGAGACTCTCTGACAGCTGCTGCAAGTCCGCAATCTCATTTTCACTGAT 2159
OY 2161 CAGGATGTTGTTGCGAGCGTTGGAATGACACAGATGCAATGCTATGTA 2220
Db 2160 CAGGATGTTGTTGCGAGCGTTGGAATGACACAGATGCAATGCTATGTA 2219
OY 2221 CTTTGTGAAGGAGAAATGCTGAAAAAAGTTTGAATAATTTGAAAAATTCGCGAGAA 2280
Db 2220 CTTTGTGAAGGAGAAATGCTGAAAAAAGTTTGAATAATTTGAAAAATTCGCGAGAA 2279
OY 2281 AGGTGGCAAAAAACATTTGCAAAATTTGTTTCTTTCAGAAATTCGCAAAACT 2340
Db 2280 AGGTGGCAAAAAACATTTGCAAAATTTGTTTCTTTCAGAAATTCGCAAAACT 2339
OY 2341 TGGTCAAAAAATGCGCATTAATGCTGTTTGAAGTTTCCATTAATAACACGAA 2400
Db 2340 TGGTCAAAAAATGCGCATTAATGCTGTTTGAAGTTTCCATTAATAACACGAA 2399
OY 2401 TTTTATCCCGGATTTGATTTTGTGTAATTAATGAGAAATTTACGAATTCG 2460
Db 2400 TTTTATCCCGGATTTGATTTTGTGTAATTAATGAGAAATTTACGAATTCG 2459
OY 2461 ATTAATAACGTTATTTTCTATTCGAATTTTAAAGCATATTTTCTTCTGATTTGATTT 2520
Db 2460 ATTAATAACGTTATTTTCTATTCGAATTTTAAAGCATATTTTCTTCTGATTTGATTT 2519
OY 2521 GCGAAAGATGCTGATTTTCAAAAAATGCTTTTAAATGTAATAATTTGAAAAAT 2580
Db 2520 GCGAAAGATGCTGATTTTCAAAAAATGCTTTTAAATGTAATAATTTGAAAAAT 2579
OY 2581 ACATTAATAATGATTTTGAATTTTCTTGAATAACAGGTTTCTGCTGATTTGC 2640
Db 2580 ACATTAATAATGATTTTGAATTTTCTTGAATAACAGGTTTCTGCTGATTTGC 2639
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Qy	2641	TGACGAAAAACCCCAAAATTCATTTTGCACATTAATAAAAAACAGAAAAATCGTTTTT	2700
Db	2640	TGACGAAAAAACCCCAAAATTCATTTTGCACATTAATAAAAAACAGAAAAATCGTTTTT	2699
Qy	2701	TAAAGCTTAATTTTCCGCCAGAAATGACGAAATTAATTTGCAAAATTTCTAATTTTCAGATA	2760
Db	2700	TAAAGCTTAATTTTCCGCCAGAAATGACGAAATTAATTTGCAAAATTTCTAATTTTCAGATA	2759
Qy	2761	GGTCATAATCTGTTGGGGGGTTTGTAGCTGCAAAAATGATGAAATCCGTGGAACTGCGAG	2820
Db	2760	GGTCATAATCTGTTGGGGGGTTTGTAGCTGCAAAAATGATGAAATCCGTGGAACTGCGAG	2819
Qy	2821	GGACAAAGTGGGAAACCTCTTGTCTTAAACAATCGCGCTTCATCAAAAGCGCGATCCGCAAC	2880
Db	2820	GGACAAAGTGGGAAACCTCTTGTCTTAAACAATCGCGCTTCATCAAAAGCGCGATCCGCAAC	2879
Qy	2881	AACGTGAAGGAAACACAAATGGAAGCTGGGTAAAGAGATTTTGCATAGACATTTAGAACTCAA	2940
Db	2880	AACGTGAAGGAAACACAAATGGAAGCTGGGTAAAGAGATTTTGCATAGACATTTAGAACTCAA	2939
Qy	2941	TATCCCCCTTTCCCTAGTACCTTGACTTCCCGGGGTGTGGTAAAGCCGAAATTAACAG	3000
Db	2940	TATCCCCCTTTCCCTAGTACCTTGACTTCCCGGGGTGTGGTAAAGCCGAAATTAACAG	2999
Qy	3001	GTTGGGTAGCCTCTGGGGGGGACGTGGAAACATTTCAAGTAAATTAAGTATTAGTTATGAT	3060
Db	3000	GTTGGGTAGCCTCTGGGGGGGACGTGGAAACATTTCAAGTAAATTAAGTATTAGTTATGAT	3059
Qy	3061	AATGTTATTTGTAACGGGAATCAAAATTTGCGAAGTGTATTTTCAACAATATTGACGC	3120
Db	3060	AATGTTATTTGTAACGGGAATCAAAATTTGCGAAGTGTATTTTCAACAATATTGACGC	3119
Qy	3121	GCAAAATATCCAGTACGAGAAACTACAGTAATCTTTAAATTTTAAATTTTACAAAT	3180
Db	3120	GCAAAATATCCAGTACGAGAAACTACAGTAATCTTTAAATTTTAAATTTTACAAAT	3179
Qy	3181	AAAGAAATTAACACCTAATCAAAAAGAAATTAATTTCAAAAATCGAGCCGTAAATGACAT	3240
Db	3180	AAAGAAATTAACACCTAATCAAAAAGAAATTAATTTCAAAAATCGAGCCGTAAATGACAT	3239
Qy	3241	ACAGTAGGCAATTTAAAGAAATTAAGTATTTTCCGTACAGAGTAAATTCGCGCTCAAAAT	3300
Db	3240	ACAGTAGGCAATTTAAAGAAATTAAGTATTTTCCGTACAGAGTAAATTCGCGCTCAAAAT	3299
Qy	3301	GTTGTGAATACGCAATTCACGGAATTTTGTGTCCCGGAAATATGCTTAAAGCATTAAT	3360
Db	3300	GTTGTGAATACGCAATTCACGGAATTTTGTGTGTCCCGGAAATATGCTTAAAGCATTAAT	3359
Qy	3361	TGTGAAATTAATAAATATCAAGAAAAAATTTGACAGACATTTATATACACTGGGAAAAACA	3420
Db	3360	TGTGAAATTAATAAATATCAAGAAAAAATTTGACAGACATTTATATACACTGGGAAAAACA	3419
Qy	3421	ATGAAGAAGGACATCGAAGACGAGCAAGAAAGTGAAGAAAGTGGACGGCGGAGACAGAACGA	3480
Db	3420	ATGAAGAAGGACATCGAAGACGAGCAAGAAAGTGAAGAAAGTGGAGCGCGGAGACAGAACGA	3479
Qy	3481	CGGTGTGATGATTTGGCGCTGGAATACAGCTGACGCCATTTGGAATGTTGGAGTCTGC	3540
Db	3480	CGGTGTGATGATTTGGCGCTGGAATACAGCTGACGCCATTTGGAATGTTGGAGTCTGC	3539
Qy	3541	GGGTGTGGCGGATGATGTTGAGTTGAGTTAAGTAACTGATTCATTTGTGTAATTAATTAAT	3600
Db	3540	GGGTGTGGCGGATGATGTTGAGTTGAGTTAAGTAACTGATTCATTTGTGTAATTAATTAAT	3599
Qy	3601	TTATGTACAACTCTTACATTTGAATCTCAATTTTGTCACTGATCTCTCAATCTTTTGA	3660
Db	3600	TTATGTACAACTCTTACATTTGAATCTCAATTTTGTCACTGATCTCTCAATCTTTTGA	3659
Qy	3661	ACTGGAAGAAGTGGGAAAGCTAGGCCCAAAATTAAGGCTCTGCTGTGATTAAGATTAAT	3720
Db	3660	ACTGGAAGAAGTGGGAAAGCTAGGCCCAAAATTAAGGCTCTGCTGTGATTAAGATTAAT	3719

QY	3721	TACGCAATTTTTCGGATTTGGCTTTTGTGGCGAAACCCATCTCCGCGTAATATCA	3780
Db	3720	TACGCAATTTTTCGGATTTGGCTTTTGTGGCGAAACCCATCTCCGCGTAATATCA	3779
QY	3781	ACTTTCCGGTCTCTACATTTGCAAAAACCCGTGAACCCCTAACTTTTCTCGCCGTG	3840
Db	3780	ACTTTCCGGTCTCTACATTTGCAAAAACCCGTGAACCCCTAACTTTTCTCGCCGTG	3839
QY	3841	GCCTAGCCTCCGCTTCTCTCCACATTTCCAAAGTACCCTGTATCTCAATATTATC	3900
Db	3840	GCCTAGCCTCCGCTTCTCTCCACATTTCCAAAGTACCCTGTATCTCAATATTATC	3899
QY	3901	TTCCACTTAACGTGCTTTTGCGTGCGCTTCCCAACTCCGCCAAATTCCTGTACCG	3960
Db	3900	TTCCACTTAACGTGCTTTTGCGTGCGCTTCCCAACTCCGCCAAATTCCTGTACCG	3959
QY	3961	GTACGCGACTTGTATTTATTTTTCAAAATGTTTCTGTCTACAAACAAAATAAAC	4020
Db	3960	GTACGCGACTTGTATTTATTTTTCAAAATGTTTCTGTCTACAAACAAAATAAAC	4019
QY	4021	GGTTCCTTTTATTCACACCTTTTTCGGAACGAAACCTGCAATTTGTATATAGCGTCCG	4080
Db	4020	GGTTCCTTTTATTCACACCTTTTTCGGAACGAAACCTGCAATTTGTATATAGCGTCCG	4079
QY	4081	AAGAGATCCGGTTTTCATTTTGGCATACGTCATCCAAAAGATTAGTAGAAATA	4140
Db	4080	AAGAGATCCGGTTTTCATTTTGGCATACGTCATCCAAAAGATTAGTAGAAATA	4139
QY	4141	TCATTTTAAATATATATATATCATCTTTCTCGCCTCTCTGTCTGAGACGCGTCAAT	4200
Db	4140	TCATTTTAAATATATATATATCATCTTTCTCGCCTCTCTGTCTGAGACGCGTCAAT	4199
QY	4201	TGCGATGCGCTTGAAATTTTTCGAAACAAAAGTTTGTAGTAAAGATGCCCCC	4260
Db	4200	TGCGATGCGCTTGAAATTTTTCGAAACAAAAGTTTGTAGTAAAGATGCCCCC	4259
QY	4261	GCCTTATGCGTTTTCACCATCAGATAGCTCCGCATTTGATTCCTTGATTTTGTG	4320
Db	4260	GCCTTATGCGTTTTCACCATCAGATAGCTCCGCATTTGATTCCTTGATTTTGTG	4319
QY	4321	GTATATTAACAAAACGTTAGTGGACGATTAACAAAACAACATGCGTCTTACTAT	4380
Db	4320	GTATATTAACAAAACGTTAGTGGACGATTAACAAAACAACATGCGTCTTACTAT	4379
QY	4381	TCACCTCTGTTGCTTCTTTGGCTTTGGCTTTGTGAGCGAAAGACATATCACTG	4440
Db	4380	TCACCTCTGTTGCTTCTTTGGCTTTGGCTTTGTGAGCGAAAGACATATCACTG	4439
QY	4441	TCGAAGGTCACATTTTGTATTAAGAAGATTCAGAGAGAGTTCCTTGGGAGAA	4500
Db	4440	TCGAAGGTCACATTTTGTATTAAGAAGATTCAGAGAGAGTTCCTTGGGAGAA	4499
QY	4501	AGATACGTGTGAGTTTTCAGTCTGTTTACCTTGAAGCGCTTAAAAAGACTAAAAAG	4560
Db	4500	AGATACGTGTGAGTTTTCAGTCTGTTTACCTTGAAGCGCTTAAAAAGACTAAAAAG	4559
QY	4561	CCTAAAAATGAGTTTTCACACCTGTTTAAAAAGAAAGCCGAATTTGCACAGCTTTAC	4620
Db	4560	CCTAAAAATGAGTTTTCACACCTGTTTAAAAAGAAAGCCGAATTTGCACAGCTTTAC	4619
QY	4621	GATATTTTCATATTTGTATTTGAATTTTATATCATCTCCCAACGTTCTTTAC	4680
Db	4620	GATATTTTCATATTTGTATTTGAATTTTATATCATCTCCCAACGTTCTTTAC	4679
QY	4681	GAAATTTTGCATTTTGTAGCTTAAATAGATACCTGGTCTGGACACGAACATTTTG	4740
Db	4680	GAAATTTTGCATTTTGTAGCTTAAATAGATACCTGGTCTGGACACGAACATTTTG	4739
QY	4741	TTAAATTCAAAAGATGCGCGCTTTAAAGAGTCTTACTAGTTGAACCTCTGTGTGC	4800
Db	4740	TTAAATTCAAAAGATGCGCGCTTTAAAGAGTCTTACTAGTTGAACCTCTGTGTGC	4799
QY	4801	GGACTTTTCATGATTTTTCGTAGCGCTTTTATTAAGAAAATGTATTTATTTATCA	4860

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Db 4800 GGAATTTTATGATTTTCTAGCGTTTATTAAGAAAATGATTTATTTATCA 4859
QY 4861 AATTTTATTTTACCAATCGGAAAAACAAATGAGAACCGGATTAATAATTCGAG 4920
Db 4860 AATTTTATTTTACCAATCGGAAAAACAAATGAGAACCGGATTAATAATTCGAG 4919
QY 4921 CAACAATAGTTGAAATTAAGTACTCTTTTAAAGGNNCATTCTATATTTACAC 4980
Db 4920 CAACAATAGTTGAAATTAAGTACTCTTTTAAAGGNNCATTCTATATTTACAC 4919
QY 4981 AACTGTGTGCGNNNGGATCGCATTTTGAAGCAAAATTCAGAAATTCAT 5040
Db 4980 AACTGTGTGCGNNNGGATCGCATTTTGAAGCAAAATTCAGAAATTCAT 5039
QY 5041 ATATGTTCAAAAACCAATATGCGAATTTCAAGCTTGAAGCAAAATTCAGAAAT 5100
Db 5040 ATATGTTCAAAAACCAATATGCGAATTTCAAGCTTGAAGCAAAATTCAGAAAT 5099
QY 5101 TCTAAAAATTTAAAAAATCCTTGGAATGTGAATTTGATTCACACTGGAAGTCAT 5160
Db 5100 TCTAAAAATTTAAAAAATCCTTGGAATGTGAATTTGATTCACACTGGAAGTCAT 5159
QY 5161 ATGCAAAATTTGCTATTTCCGNNNTGANNATTTGTCCAGCTGCGCGCAAAAGAG 5220
Db 5160 ATGCAAAATTTGCTATTTCCGNNNTGANNATTTGTCCAGCTGCGCGCAAAAGAG 5219
QY 5221 AAAGCAGANNACGATTTCTGGCAATTTTCTGCTACCGTGTCAATTTATTAACCTC 5280
Db 5220 AAAGCAGANNACGATTTCTGGCAATTTTCTGCTACCGTGTCAATTTATTAACCTC 5219
QY 5281 TAATAGCTGATTTTCTGCTATTTGCAACTGATTCATTAATTTGCAATTTAA 5340
Db 5280 TAATAGCTGATTTTCTGCTATTTGCAACTGATTCATTAATTTGCAATTTAA 5339
QY 5341 TATTGACTTTGATGTGTGCTTAGAAAAAACCATAAAGCTCATAGCTTTAGGC 5400
Db 5340 TATTGACTTTGATGTGTGCTTAGAAAAAACCATAAAGCTCATAGCTTTAGGC 5399
QY 5401 TGCCAAATATATTCCTAGACATATTAATAAACCCTTAATTTCTGCAACACCTACAGC 5460
Db 5400 TGCCAAATATATTCCTAGACATATTAATAAACCCTTAATTTCTGCAACACCTACAGC 5459
QY 5461 TATCAAGCTATTTAGTATTCATTTTCCAGTCGACCCGATGACAACTGCTTCAA 5520
Db 5460 TATCAAGCTATTTAGTATTTTCAATTTTCCAGTCGACCCGATGACAACTGCTTCAA 5519
QY 5521 TGCAATGAAACAAAGAGAGTCTCACTTACCGGATCCGAGAGATCACTCCAA 5580
Db 5520 TGCAATGAAACAAAGAGAGTCTCACTTACCGGATCCGAGAGATCACTCCAA 5579
QY 5581 TCTCTCATACCTGATATATCAACCACAGTGCACAGTGAAGAGGCGGATGCAAGCGTG 5640
Db 5580 TCTCTCATACCTGATATATCAACCACAGTGCACAGTGAAGAGGCGGATGCAAGCGTG 5639
QY 5641 TTTGAGAGTATTTGATTTCCAAAGAGAGAGTGGTGAACCTTATGATATGATACGTCA 5700
Db 5640 TTTGAGAGTATTTGATTTCCAAAGAGAGAGTGGTGAACCTTATGATATGATACGTCA 5699
QY 5701 CTCTTGATATTTCTTCCGCTAAAGACAGAGAGTGTAGAAAATGTTTTTTGTTT 5760
Db 5700 CTCTTGATATTTCTTCCGCTAAAGACAGAGAGTGTAGAAAATGTTTTTTGTTT 5759
QY 5761 GGTGTTGCTTTTGAAGAGAGACTTTTATCTCTTTTAAATTCACAAATAAATATTTG 5820
Db 5760 GGTGTTGCTTTTGAAGAGAGACTTTTATCTCTTTTAAATTCACAAATAAATATTTG 5819
QY 5821 GAAACCGTTGAATTTTAACTTTGAACTGTAGAAAAGTGGTATATGTTGCAAT 5880
Db 5820 GAAACCGTTGAATTTTAACTTTGAACTGTAGAAAAGTGGTATATGTTGCAAT 5879
QY 5881 TTTGCAAGTATATCTTTGTGATATCAGAAATTAACGAAGTCAAGCAAAATATTTAGC 5940

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Db 5880 TTTGCAAGTATATCTTTGTGATATCAGAAATTAACGAATCAAGCAGCAATTTAGC 5939
QY 5941 GAAACCAAAATTTATGAGATGCGACATATTTGACCGCAAAATATCTGTAGCGAAA 6000
Db 5940 GAAACCAAAATTTATGAGATGCGACATATTTGACCGCAAAATATCTGTAGCGAAA 5999
QY 6001 CTACAGTATTTCTCAAAAGACTAGTACGCTGTGATTTAGAGCTGATTTTG 6060
Db 6000 CTACAGTATTTCTCAAAAGACTAGTACGCTGTGATTTAGAGCTGATTTTG 6059
QY 6061 AATGAATCAGACTAGAGAGAGAGAGAAATTTGAACATCAATTTGAACATTTCA 6120
Db 6060 AATGAATCAGACTAGAGAGAGAGAGAAATTTGAACATCAATTTGAACATTTCA 6119
QY 6121 AAAAGTGAACCTTGTACTAGTACTGTTCTTAAAGATTTACTGTGTTTGGCTACGAG 6180
Db 6120 AAAAGTGAACCTTGTACTAGTACTGTTCTTAAAGATTTACTGTGTTTGGCTACGAG 6179
QY 6181 ATATTTGNGNGTCAAAATATGTTGNGCAATACGATCTCAGAAATGTTGTTCTGTAA 6240
Db 6180 ATATTTGNGNGTCAAAATATGTTGNGCAATACGATCTCAGAAATGTTGTTCTGTAA 6239
QY 6241 TGTCTTGAATTTTCCATTTCAACATCAATTAAGCAATCTAAAAATGTGGGTTCTGCA 6300
Db 6240 TGTCTTGAATTTTCCATTTCAACATCAATTAAGCAATCTAAAAATGTGGGTTCTGCA 6299
QY 6301 GCGACCACTATGACTGATGCTGAGGCAAGCCACCTCAAAAACCTACGTTCTTAA 6360
Db 6300 GCGACCACTATGACTGATGCTGAGGCAAGCCACCTCAAAAACCTACGTTCTTAA 6359
QY 6361 CAATACATTTTAAATATGATATTAATAAATTTGTTGCTAGCAAGTACGCTTAA 6420
Db 6360 CAATACATTTTAAATATGATATTAATAAATTTGTTGCTAGCAAGTACGCTTAA 6419
QY 6421 TTTGAGTCAACACTTTCTAATTTAATGCGGCTTCAAAAAGTCTTTCTTGAANA 6480
Db 6420 TTTGAGTCAACACTTTCTAATTTAATGCGGCTTCAAAAAGTCTTTCTTGAANA 6479
QY 6481 TATTAAGCTTTTATATTTATTAATAAATTTGATATGATATCAAAAGGACTA 6540
Db 6480 TATTAAGCTTTTATATTTATTTATTAATAAATTTGATATGATATCAAAAGGACTA 6539
QY 6541 GTTTGATTAATAATTTATCA 6560
Db 6540 GTTTGATTAATAATTTATCA 6559

```

RESULT 3
 US-08-288-295-1
 ; Sequence 1, Application US/08288295
 ; GENERAL INFORMATION:
 ; APPLICANT: Horvitz, H. Robert
 ; APPLICANT: Hengartner, Michael
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 ; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FISH & RICHARDSON
 ; STREET: 225 Franklin Street, Suite 3100
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A. (F) ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/288,295
 ; FILING DATE: 10-AUG-1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/927,681
FILING DATE: 10-AUG-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 01997/201003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6559 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-285-1

Query Match 99.5%; Score 6529.8; DB 6; Length 6559;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6559; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATCGATGTCGTCCCAATGATGATTTCCGATTTCTCAGTACATGCTCACAATTTA 60
DB 1 ATCGATGTCGTCCCAATGATGATTTCCGATTTCTCAGTACATGCTCACAATTTA 60
QY 61 CAAAATCTCGAAGAAAGAAAGATGCAAGAGATGCAAGAGTTCGGAATCTAAATTTT 120
DB 61 CAAAATCTCGAAGAAAGAAAGATGCAAGAGATGCAAGAGTTCGGAATCTAAATTTT 120
QY 121 TAAATTTAAAAAATCAATTTGCAATTTGAATTCAGTCTCAGTCTGTTTGAATGCAA 180
DB 121 TAAATTTAAAAAATCAATTTGCAATTTGAATTCAGTCTCAGTCTGTTTGAATGCAA 180
QY 181 TCCCTTAAGTAACTCTGATGTCGCCATTTCTCCAGAAATTCCTTCAAGTAGTGTT 240
DB 181 TCCCTTAAGTAACTCTGATGTCGCCATTTCTCCAGAAATTCCTTCAAGTAGTGTT 240
QY 241 TTGCTAGTATTTCTCGCGCAAGAAATAGAACTTTGCAATCTCTGAGCGAAACGGGAT 300
DB 241 TTGCTAGTATTTCTCGCGCAAGAAATAGAACTTTGCAATCTCTGAGCGAAACGGGAT 300
QY 301 TTTTNTAACAAGAAATCTGAGCAAGCAATAGACTTTTCAATATTCCTTATTTGG 360
DB 301 TTTTNTAACAAGAAATCTGAGCAAGCAATAGACTTTTCAATATTCCTTATTTGG 360
QY 361 CTGTCCATTTGGAAGCAACCAATCTTTAAGCTGTCCAGCGAGAAAGTCTCCACTGCCA 420
DB 361 CTGTCCATTTGGAAGCAACCAATCTTTAAGCTGTCCAGCGAGAAAGTCTCCACTGCCA 420
QY 421 AGATTAAGAGCTAATTTTGAAGCCGAATTTTACTAAATCTAGCCATGAGTGGAT 480
DB 421 AGATTAAGAGCTAATTTTGAAGCCGAATTTTACTAAATCTAGCCATGAGTGGAT 480
QY 481 GGATGAGAAATTCGAGAAATTTAGATTTTCAATCTGGAATTTGCAATGGAATTAAT 540
DB 481 GGATGAGAAATTCGAGAAATTTAGATTTTCAATCTGGAATTTGCAATGGAATTAAT 540
QY 541 ATTCAAGAAATTCAGAGAAATTCAGCAAAATTAATTAATTAATTAATTAATTAAT 600
DB 541 ATTCAAGAAATTCAGAGAAATTCAGCAAAATTAATTAATTAATTAATTAATTAAT 600
QY 601 GAAAGTGGCGCGGCTGTTGCTGAGCAATCTTCAAGAGAGCGCTGCTGGCGG 660
DB 601 GAAAGTGGCGCGGCTGTTGCTGAGCAATCTTCAAGAGAGCGCTGCTGGCGG 660
QY 661 ACTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 661 ACTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 CCGCCCTGTTCTTTTCAATTTTGAATTAAGAAATTCAGCATTTGTTTCAAGATGTTAAC 780

DB 720 CCGCCCTGTTCTTTTCAATTTTGAATTAAGAAATTCAGCATTTGTTTCAAGATGTTAAC 779
QY 781 ATTCACATGCGATTTCTGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
DB 781 ATTCACATGCGATTTCTGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 839
QY 841 ACATGATGCTGACCAAGAGTGGGATTTTGAATTTTCCGTAATTAATTAATTAATTAAT 900
DB 841 ACATGATGCTGACCAAGAGTGGGATTTTGAATTTTCCGTAATTAATTAATTAATTAAT 899
QY 901 TGTGATGCGATGAGAGAAATGATATAACAGACATTTCTTCAATTAATTAATTAATTA 960
DB 901 TGTGATGCGATGAGAGAAATGATATAACAGACATTTCTTCAATTAATTAATTAATTA 959
QY 961 TATTCACAGTCCGAGGCAAAACAGCCATTCAGAAAGTGGGATGAGATACCTGTTGAAG 1020
DB 961 TATTCACAGTCCGAGGCAAAACAGCCATTCAGAAAGTGGGATGAGATACCTGTTGAAG 1019
QY 1021 CAGCGCTCCAGAAATCGCCCAATCGCTCCAGATTCACCGCTTACACCAATTTGACG 1080
DB 1021 CAGCGCTCCAGAAATCGCCCAATCGCTCCAGATTCACCGCTTACACCAATTTGACG 1079
QY 1081 TGGATGCTCTCCGATTTCCATGATGATGATGATGATGATGATGATGATGATGATG 1140
DB 1081 TGGATGCTCTCCGATTTCCATGATGATGATGATGATGATGATGATGATGATGATG 1139
QY 1141 GGAGGAATGGAATGCGAGTTTGGCGTTGCTGATTTGATTTGATTTGATTTGATTTG 1200
DB 1141 GGAGGAATGGAATGCGAGTTTGGCGTTGCTGATTTGATTTGATTTGATTTGATTTG 1199
QY 1201 AGCTGAACTTACATGCGCGGTGACCGCTGCTTCAAGTACATGATTTTCCCATTC 1260
DB 1201 AGCTGAACTTACATGCGCGGTGACCGCTGCTTCAAGTACATGATTTTCCCATTC 1259
QY 1261 ATTTTCATGCTTTAAGCGAATTTGGCTTTAGATTTGATTTGATTTGATTTGATTTG 1320
DB 1261 ATTTTCATGCTTTAAGCGAATTTGGCTTTAGATTTGATTTGATTTGATTTGATTTG 1319
QY 1321 AATTTGAGAGGATGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1380
DB 1321 AATTTGAGAGGATGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1379
QY 1381 TTTCAGATCTAACAATGCGGATATCTGATCTGAGCTTTGCGCTGCTGCCA 1440
DB 1381 TTTCAGATCTAACAATGCGGATATCTGATCTGAGCTTTGCGCTGCTGCCA 1439
QY 1441 TTGCTTTCAACTTTGCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1500
DB 1441 TTGCTTTCAACTTTGCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1499
QY 1501 TTCTTTTCTTACTGCG 1560
DB 1501 TTCTTTTCTTACTGCG 1559
QY 1561 ATTTCTGATTTTCTCTTTTCTGATATTTACTCTCTCTCTCTCTCTCTCTCTCTCT 1620
DB 1561 ATTTCTGATTTTCTCTTTTCTGATATTTACTCTCTCTCTCTCTCTCTCTCTCTCT 1619
QY 1621 GTCTAGATGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1680
DB 1621 GTCTAGATGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1679
QY 1681 GCGGAACTGCTGAGCAATTCGCGGTATTCGCGAGCAAGATGCGACTGCGAGATG 1740
DB 1681 GCGGAACTGCTGAGCAATTCGCGGTATTCGCGAGCAAGATGCGACTGCGAGATG 1739
QY 1741 AAGAGTTTCTGGGATTAAGAGCAAGAGCCAGGATTTTGAATTAATTAATTAATTAAT 1800
DB 1741 AAGAGTTTCTGGGATTAAGAGCAAGAGCCAGGATTTTGAATTAATTAATTAATTAAT 1799
QY 1801 CAGGACTTGCATCAGGATGAGGCTTGCAGCGGAAGATGCTCATCGAGAGTCA 1860

QY 4021 GGTCTTTTATTCACCCCTTTTTCGAGCAAACTGCATTTTGAATATAGCGTGGC 4080
|||||
Db 4020 GGTCTTTTATTCACCCCTTTTTCGAGCAAACTGCATTTTGAATATAGCGTGGC 4079
QY 4081 AAGGAATCCGCTTTTCATTTTGGCCATCAGTCATCCAAAAAGTTTACTAGAAATA 4140
|||||
Db 4080 AAGGAATCCGCTTTTCATTTTGGCCATCAGTCATCCAAAAAGTTTACTAGAAATA 4139
QY 4141 TCATTTTATATATATGATTCATTTTCGCGCTCTCTGCTCGAGAGCGTCAAT 4200
|||||
Db 4140 TCATTTTATATATATGATTCATTTTCGCGCTCTCTGCTCGAGAGCGTCAAT 4199
QY 4201 TCGATGCCCTTGAATTTTTCGAAAAAAGTTTGTATGTAAACGATCCGCC 4260
|||||
Db 4200 TCGATGCCCTTGAATTTTTCGAAAAAAGTTTGTATGTAAACGATCCGCC 4259
QY 4261 GCCTTATCCGCTTTTCACCATTCAGATAGGCTCCGCAATTTGATTCCTTGAATTTTGTG 4320
|||||
Db 4260 GCCTTATCCGCTTTTCACCATTCAGATAGGCTCCGCAATTTGATTCCTTGAATTTTGTG 4319
QY 4321 GTATATAAAAAACAACAAAGCTTAGTCAGATTCAAAAACAACATGCGTCTTACTAT 4380
|||||
Db 4320 GTATATAAAAAACAACAAAGCTTAGTCAGATTCAAAAACAACATGCGTCTTACTAT 4379
QY 4381 TCACCTCTGCTTTCTTTTGGCTTTGGCTTTGGTGAAGCAAGACAGTATCAGT 4440
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Db 4380 TCACCTCTGCTTTCTTTTGGCTTTGGCTTTGGTGAAGCAAGACAGTATCAGT 4439
QY 4441 TCAAGGATACACTATTTTGAATAGAAGAAATTCAGAGGATGTTACCTTTGGAGAA 4500
|||||
Db 4440 TCAAGGATACACTATTTTGAATAGAAGAAATTCAGAGGATGTTACCTTTGGAGAA 4499
QY 4501 AGATCTCTGATTTTTCAGTCTTGTGTAGCTTGAAGCGCTTAAAAAGGATAAAAAG 4560
|||||
Db 4500 AGATCTCTGATTTTTCAGTCTTGTGTAGCTTGAAGCGCTTAAAAAGGATAAAAAG 4559
QY 4561 CCAAAAAATGAAGTTTCCACCTGTTTCAAAAGAACCCGAAATGACACCTTTACAC 4620
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Db 4560 CCAAAAAATGAAGTTTCCACCTGTTTCAAAAGAACCCGAAATGACACCTTTACAC 4619
QY 4621 GAGATTTCTCAATATTTTGTATTTGAATTTTCAATTCATCCCAACGCTTTTACAC 4680
|||||
Db 4620 GAGATTTCTCAATATTTTGTATTTGAATTTTCAATTCATCCCAACGCTTTTACAC 4679
QY 4681 GAAATTTTCCGATTTTGAAGTTAAATAGATACCTGCTCGACAGCAAACTTTTG 4740
|||||
Db 4680 GAAATTTTCCGATTTTGAAGTTAAATAGATACCTGCTCGACAGCAAACTTTTG 4739
QY 4741 TTAATTTCAAAAAAGATGGCGCTTAAAGAGTGTGTAAGAACTTCTGTTGTC 4800
|||||
Db 4740 TTAATTTCAAAAAAGATGGCGCTTAAAGAGTGTGTAAGAACTTCTGTTGTC 4799
QY 4801 GGACTTTTCATCGATTTTTCGAGCTTTTATTAAGNCAATTTTATTTATTTTCAA 4860
|||||
Db 4800 GGACTTTTCATCGATTTTTCGAGCTTTTATTAAGNCAATTTTATTTATTTTCAA 4859
QY 4861 AAATTTAATTTTACCGAATCCGCAAAAAAATAAGACACCGATAAAAATTCGAG 4920
|||||
Db 4860 AAATTTAATTTTACCGAATCCGCAAAAAAATAAGACACCGATAAAAATTCGAG 4919
QY 4921 CACATATGTTTGAATATACGATCTTTTAAAGNCAATTTTCTATATTTTCAAC 4980
|||||
Db 4920 CACATATGTTTGAATATACGATCTTTTAAAGNCAATTTTCTATATTTTCAAC 4979
QY 4981 AAATTTGCTGTGCGNCCGCGATCGTCAATTTTGAATCAAGAAATTTGCAT 5040
|||||
Db 4980 AAATTTGCTGTGCGNCCGCGATCGTCAATTTTGAATCAAGAAATTTGCAT 5039
QY 5041 AATATTTCAAAAAACCAATTTATGCGCAATTTCAAGCTTGAAGAAATTCAGAAAT 5100
|||||
Db 5040 AATATTTCAAAAAACCAATTTATGCGCAATTTCAAGCTTGAAGAAATTCAGAAAT 5099
QY 5101 TCTAAAAATTTAAAAAATCATTCGAAATGTGAATTTGATTTCAACTTGAAGTCCAT 5160
|||||

|||||
Db 5100 TCTAAAAATTTAAAAAATCATTCGAATGTGAATTTGATTTCAACTTGAAGTCCAT 5159
QY 5161 ATGCCAAATTTGCTATTTCCGNNMTTGANNATTTTGTCCAGTGGCCCGGAAAAAG 5220
|||||
Db 5160 ATGCCAAATTTGCTATTTCCGNNMTTGANNATTTTGTCCAGTGGCCCGGAAAAAG 5219
QY 5221 AAAGCAGNNACTGATTTTCCGAAATTTTTCCTGATCCGCTGCAATTTTGAACCTC 5280
|||||
Db 5220 AAAGCAGNNACTGATTTTCCGAAATTTTTCCTGATCCGCTGCAATTTTGAACCTC 5279
QY 5281 TATATAGCTGATTTTCTGATTTTGAACAATTAATCAATTAATTTGCAATTTATA 5340
|||||
Db 5280 TATATAGCTGATTTTCTGATTTTGAACAATTAATCAATTAATTTGCAATTTATA 5339
QY 5341 TATGACTTTTGAATGTGGCTTAGAAAAAACAACCAACCAATCTGCTTATGGC 5400
|||||
Db 5340 TATGACTTTTGAATGTGGCTTAGAAAAAACAACCAACCAATCTGCTTATGGC 5399
QY 5401 TGCCATATATTTCTAGGACATATTAACCCCTTAAATTTCTGCAACCTTACAGC 5460
|||||
Db 5400 TGCCATATATTTCTAGGACATATTAACCCCTTAAATTTCTGCAACCTTACAGC 5459
QY 5461 TATCAACGTAATTTAGTATTTCAATTTTCCAGTCCGACCCCGATGACAAAGTCCCTCAA 5520
|||||
Db 5460 TATCAACGTAATTTAGTATTTCAATTTTCCAGTCCGACCCCGATGACAAAGTCCCTCAA 5519
QY 5521 TGCATATGACAAAGAGAGAGTTCACCTTACCGATCCGAGACAGATCACCTCAA 5580
|||||
Db 5520 TGCATATGACAAAGAGAGAGTTCACCTTACCGATCCGAGACAGATCACCTCAA 5579
QY 5581 TCTCTCCCTTACCTATATTCACCAACAGTGCAGAGTGAAGAGCCGATGCAAGCGTG 5640
|||||
Db 5580 TCTCTCCCTTACCTATATTCACCAACAGTGCAGAGTGAAGAGCCGATGCAAGCGTG 5639
QY 5641 TTTGAGATATTTATTTCCAAAGAGAGATCGGTGACCTTATGATATGACATATCTCA 5700
|||||
Db 5640 TTTGAGATATTTATTTCCAAAGAGAGATCGGTGACCTTATGATATGACATATCTCA 5699
QY 5701 CTCTTGATATTTCTTCCGCTTAAGACAGAGAGATGCTTAAGAAATGTTTTTGTGTT 5760
|||||
Db 5700 CTCTTGATATTTCTTCCGCTTAAGACAGAGAGATGCTTAAGAAATGTTTTTGTGTT 5759
QY 5761 GGTTCGCTGTTTGAAGGAGAGCTTCTATCTCTTTAATTTCAACATTAACATTTG 5820
|||||
Db 5760 GGTTCGCTGTTTGAAGGAGAGCTTCTATCTCTTTAATTTCAACATTAACATTTG 5819
QY 5821 GAAACCGTTGAATTTTAACTTTGAACGTAAGAAAGTTGCTGATTTGTTGCAAT 5880
|||||
Db 5820 GAAACCGTTGAATTTTAACTTTGAACGTAAGAAAGTTGCTGATTTGTTGCAAT 5879
QY 5881 TTTTCCAGATATATCTTTTGGATATACAAATTAAGCAATCAAGCAGCAAAATTTAGC 5940
|||||
Db 5880 TTTTCCAGATATATCTTTTGGATATACAAATTAAGCAATCAAGCAGCAAAATTTAGC 5939
QY 5941 GAAACCAAAAAATTAATAGATGGCAACATTTTGAACGCAAAAAATTTCTGTAAGGAAA 6000
|||||
Db 5940 GAAACCAAAAAATTAATAGATGGCAACATTTTGAACGCAAAAAATTTCTGTAAGGAAA 5999
QY 6001 CTACAGTAATTTCTTCAAAAGACTAGCTGATGCGCTGTGATTTAGAGCTGCAATTTTG 6060
|||||
Db 6000 CTACAGTAATTTCTTCAAAAGACTAGCTGATGCGCTGTGATTTAGAGCTGCAATTTTG 6059
QY 6061 AAATGATTCAGACTAGAGAAAGAGGAGAAATATTGAACATCAATTGCAATTTCA 6120
|||||
Db 6060 AAATGATTCAGACTAGAGAAAGAGGAGAAATATTGAACATCAATTGCAATTTCA 6119
QY 6121 AAAAGTCAACCTTACTAGTACTAGTCTTTTAAAGATTTAGTGTGCTGTAAGAG 6180
|||||
Db 6120 AAAAGTCAACCTTACTAGTACTAGTCTTTTAAAGATTTAGTGTGCTGTAAGAG 6179
QY 6181 ATATTTTGGNGTCAAAATATGTTGNCATATAGCATCTCAGAAATTTGTGTTCTGTA 6240
|||||

Db 6180 ATATTTGNGNGTCAATATGTTGNGCAATACCATCTCAGATTGTGTCTGTCA 6239
Qy 6241 TGTCTGAAAAATTTCCATTTCAACATCAATTAAGCAAAATCTAAAAATGTGGTTCTGA 6300
Db 6240 TGTCTGAAAAATTTCCATTTCAACATCAATTAAGCAAAATCTAAAAATGTGGTTCTGA 6299
Qy 6301 GCGACCCATGACTGTGATCGTGGCAAGCCACCTCAGAAAACCTGCTCTTAA 6360
Db 6300 GCGACCCATGACTGTGATCGTGGCAAGCCACCTCAGAAAACCTGCTCTTAA 6359
Qy 6361 CAATTAATTTTATGATTTAGTATGATTTAATAATTTGCTGCTAGCTAGCTGCTT 6420
Db 6360 CAATTAATTTTATGATTTAGTATGATTTAATAATTTGCTGCTAGCTAGCTGCTT 6419
Qy 6421 TTTAGTGCAGCAACTCTTAATTTAATCGCGGTCTTCAAAAAGTCTTTTGA 6480
Db 6420 TTTAGTGCAGCAACTCTTAATTTAATCGCGGTCTTCAAAAAGTCTTTTGA 6479
Qy 6481 TATAAGCTTTATATTTATTTAATAATTTGATTCATGATTCAGAAAGCGCTA 6540
Db 6480 TATAAGCTTTATATTTATTTAATAATTTGATTCATGATTCAGAAAGCGCTA 6539
Qy 6541 GTTGTATAAAAATTTATCAA 6560
Db 6540 GTTGTATAAAAATTTATCAA 6559

RESULT 4
: Sequence 1, Application US/08801248
: GENERAL INFORMATION:
: APPLICANT: Horvitz, H. Robert
: APPLICANT: Hengartner, Michael
: TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
: TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
: NUMBER OF SEQUENCES: 8
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FISH & RICHARDSON
: STREET: 225 Franklin Street, Suite 3100
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WordPerfect 5.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/801,248
: FILING DATE: 19-FEB-1997
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/288,295
: FILING DATE: 10-AUG-1994
: APPLICATION NUMBER: US 07/927,681
: FILING DATE: 10-AUG-1992
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,162
: REFERENCE/DOCKET NUMBER: 01997/201003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-5070
: TELEFAX: (617) 542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6559 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-801-248-1
Query Match 99.5%; Score 6529.8; DB 12; Length 6559;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6559; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 ATCGATAGTCGACCAATGATTTTCCGATTTTCTCACTAGTCCATGGCTCACAATTTA 60
Db 1 ATCGATAGTCGACCAATGATTTTCCGATTTTCTCACTAGTCCATGGCTCACAATTTA 60
Qy 61 CAAAAATCGCAAAAAAGAAAGATGCAAGAGATGAAAGAGTTCCGATATTAATATT 120
Db 61 CAAAAATCGCAAAAAAGAAAGATGCAAGAGATGAAAGAGTTCCGATATTAATATT 120
Qy 121 TATTTTAAAAAAATCAATTTGCAATTTGCAATTTCACTCTCTCTGTTTGAAGTCCAA 180
Db 121 TATTTTAAAAAAATCAATTTGCAATTTGCAATTTCACTCTCTCTGTTTGAAGTCCAA 180
Qy 181 TCTTTAAGTAACCTTCTGATCGCCATTTCTTCAGAAATTCCTTCAAGTAGTGGTT 240
Db 181 TCTTTAAGTAACCTTCTGATCGCCATTTCTTCAGAAATTCCTTCAAGTAGTGGTT 240
Qy 241 TGTACTGATTTCTCTCCGCAAGATAGCACTTTCTGATTTCTCTGAGCGCAAGCGGAT 300
Db 241 TGTACTGATTTCTCTCCGCAAGATAGCACTTTCTGATTTCTCTGAGCGCAAGCGGAT 300
Qy 301 TTTTATACAAAAAAATCTATCCAGACCAACCATAGACCTTTTCAATATTTCTTATTTGG 360
Db 301 TTTTATACAAAAAAATCTATCCAGACCAACCATAGACCTTTTCAATATTTCTTATTTGG 360
Qy 361 CTGTCCATTTTGAAGACCCCAATCTTTAAGCTGTCCAGCCAGAAAGTCTCAGTCCGCA 420
Db 361 CTGTCCATTTTGAAGACCCCAATCTTTAAGCTGTCCAGCCAGAAAGTCTCAGTCCGCA 420
Qy 421 AGATTAAGGCTCATTTTGAAGCCGATTTTACTAAATCTTACCATGAGTGCAT 480
Db 421 AGATTAAGGCTCATTTTGAAGCCGATTTTACTAAATCTTACCATGAGTGCAT 480
Qy 481 GGATCAGAAATTTGAGAAATTTAGATTTTCACTTGAATTTGCAATGGAATAATTT 540
Db 481 GGATCAGAAATTTGAGAAATTTAGATTTTCACTTGAATTTGCAATGGAATAATTT 540
Qy 541 ATTCAAGAAATTCACAGAAATTCACAGAAATTTCAAGAAATTTCAAGAAATTCAGT 600
Db 541 ATTCAAGAAATTCACAGAAATTCACAGAAATTTCAAGAAATTTCAAGAAATTCAGT 600
Qy 601 GAAAAGTGGCGCGCGGCTGTTTCTGACGATCTTCAAGCAGAGCGCTGCTGGCG 660
Db 601 GAAAAGTGGCGCGCGGCTGTTTCTGACGATCTTCAAGCAGAGCGCTGCTGGCG 659
Qy 661 ACTTCTGTCCTGTCGCTGTCGATTTCCGCAAAATTCACACCTGTTTGAAGCGCA 720
Db 661 ACTTCTGTCCTGTCGCTGTCGATTTCCGCAAAATTCACACCTGTTTGAAGCGCA 719
Qy 721 CCGCCCTGTTTCTTTTCAATTTTGAATTAAGAAATCAGATGTTCCGATGATTAAC 780
Db 721 CCGCCCTGTTTCTTTTCAATTTTGAATTAAGAAATCAGATGTTTCCGATGATTAAC 779
Qy 781 ATTCCAACTGCGATTTCTGTCGCTGTTGGCGCAGATTCGATTTCCGCTCTTTGA 840
Db 781 ATTCCAACTGCGATTTCTGTCGCTGTTGGCGCAGATTCGATTTCCGCTCTTTGA 839
Qy 841 ACATCGATCGTACCAAGTGGGATTTTGAATTTTCCGTAATTTGTTGATTTT 900
Db 841 ACATCGATCGTACCAAGTGGGATTTTGAATTTTCCGTAATTTGTTGATTTT 899
Qy 901 TGTGTACGATGAAGGAATGATTAAGACACATTTCTTCAATTAATTTATATA 960
Db 901 TGTGTACGATGAAGGAATGATTAAGACACATTTCTTCAATTAATTTATATA 959
Qy 961 TATTCACAGTCCGAGCAAGACCAATCCAGAAATTCGATGGAATACCTGTTGAAG 1020
Db 961 TATTCACAGTCCGAGCAAGACCAATCCAGAAATTCGATGGAATACCTGTTGAAG 1020

Dh 960 TATTACAGTCCGAGCAAGACCCTCAATCCAGAGTTCCGATGGAATACCTGTTGAAG 1019
Qy 1021 CAGGCTCCCAAGAAATCGCCCAATGCTCCACATCTCACCCGTCACCAACCAATGATGAC 1080
Dh 1020 CAGGCTCCCAAGAAATCGCCCAATGCTCCACATCTCACCCGTCACCAACCAATGATGAC 1079
Qy 1081 TGGATGCTCTCCGATTCATAGATACAGCGGTTGTATATGCGCGGAACCTTCTGTC 1140
Dh 1080 TGGATGCTCTCCGATTCATAGATACAGCGGTTGTATATGCGCGGAACCTTCTGTC 1139
Qy 1141 GGAGAAATCGGATTCGAGTTTGCCTGATTTCAACCGCTTTGGGATTCATCCGT 1200
Dh 1140 GGAGAAATCGGATTCGAGTTTGCCTGATTTCAACCGCTTTGGGATTCATCCGT 1199
Qy 1201 AGCTGGAATTCACATGCGCGGTCAGCGCTGCTTCAAGTACATCATTTGCTTCCCATC 1260
Dh 1200 AGCTGGAATTCACATGCGCGGTCAGCGCTGCTTCAAGTACATCATTTGCTTCCCATC 1259
Qy 1261 ATTTTCCATCTCTTAACGGAATTCGCTTCTTACGATTCGATTTGGCTAAGGAGTCAAT 1320
Dh 1260 ATTTTCCATCTCTTAACGGAATTCGCTTCTTACGATTCGATTTGGCTAAGGAGTCAAT 1319
Qy 1321 AATGTGAGACAGTAGAGATTGAATTAATTAATTTAAATATAATTAATTAAT 1380
Dh 1320 AATGTGAGACAGTAGAGATTGAATTAATTAATTTAAATATAATTAATTAAT 1379
Qy 1381 TTCAGATCTACAATCGGAGATCTCGATCTGATCGACTTGGGCTAATCTTGCCTCGCA 1440
Dh 1380 TTCAGATCTACAATCGGAGATCTCGATCTGATCGACTTGGGCTAATCTTGCCTCGCA 1439
Qy 1441 TTGCTCTTACTCTTGGCAGACAAGACAAGCAAGACTGCTTACGAGACAGATGCTCGCC 1500
Dh 1440 TTGCTCTTACTCTTGGCAGACAAGACAAGCAAGACTGCTTACGAGACAGATGCTCGCC 1499
Qy 1501 TTCTTTTCTTACTCCGCCCCAGCCCTCGACATCTCTGATTTACTTTACTTTTACCTTG 1560
Dh 1500 TTCTTTTCTTACTCCGCCCCAGCCCTCGACATCTCTGATTTACTTTACTTTTACCTTG 1559
Qy 1561 ATTTCTTGATTTTCTCTCTTCTTCCGTAGATTTACTCTCTCTCTCTTCTTCTTCTCT 1620
Dh 1560 ATTTCTTGATTTTCTCTCTTCTTCCGTAGATTTACTCTCTCTCTCTCTTCTTCTCT 1619
Qy 1621 GTCTAGAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1680
Dh 1620 GTCTAGAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1679
Qy 1681 GCGACAACCTCGAGGAATCGGCGGTATCGGAGCAAGATGCGGAGCTGGGAGATG 1740
Dh 1680 GCGACAACCTCGAGGAATCGGCGGTATCGGAGCAAGATGCGGAGCTGGGAGATG 1739
Qy 1741 AAGGAGTTTCTGGGATTAAGAGCAGAGAGCCACGATTTTGGATCAATAGTATGCT 1800
Dh 1740 AAGGAGTTTCTGGGATTAAGAGCAGAGAGCCACGATTTTGGATCAATAGTATGCT 1799
Qy 1801 CAGGACTTGCATACCGAGTAGAGCAGGCTTGAAGGCAAGATGTCATCGAGATCA 1860
Dh 1800 CAGGACTTGCATACCGAGTAGAGCAGGCTTGAAGGCAAGATGTCATCGAGATCA 1859
Qy 1861 ATTATGGAATAATCAATGATTTGGGAGAGAGCAAGGCTTATATCGAGGATTTGTGTA 1920
Dh 1860 ATTATGGAATAATCAATGATTTGGGAGAGAGCAAGGCTTATATCGAGGATTTGTGTA 1919
Qy 1921 ATTTTAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1980
Dh 1920 ATTTTAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1979
Qy 1981 CACCGAATCCGGCAAAACGAGATGAATGTTTGGAGACACCGGATTCGCTGGAGTG 2040
Dh 1980 CACCGAATCCGGCAAAACGAGATGAATGTTTGGAGACACCGGATTCGCTGGAGTG 2039
Qy 2041 CAACCGGAGCAGAAATGATGCGATTAAGGAACGATTTTCAGAGAAGACACGCGGAA 2100
Dh 2040 CAACCGGAGCAGAAATGATGCGATTAAGGAACGATTTTCAGAGAAGACACGCGGAA 2099

Qy 2101 AATTTGAGACCTTCTGTAGAGAGCTGTGCGAGTCCGAGATTCATTTTCACTGAT 2160
Dh 2100 AATTTGAGACCTTCTGTAGAGAGCTGTGCGAGTCCGAGATTCATTTTCACTGAT 2159
Qy 2161 CAGGATGTGTTGCGAGGTTGGAATVGCAGACAGATCAATGTCCATGTCTATGGA 2220
Dh 2160 CAGGATGTGTTGCGAGGTTGGAATVGCAGACAGATCAATGTCTATGGA 2219
Qy 2221 CGTTTGTAAAGGAGAAATTAATGAAAAAGTTGCAAAATTCGAAATTCGCGAGAA 2280
Dh 2220 CGTTTGTAAAGGAGAAATTAATGAAAAAGTTGCAAAATTCGAAATTCGCGAGAA 2279
Qy 2281 AGGTGCGAGAAAAACATTTGCAAAATTTGTTTCTTCCAGAAATTCAGAAAACT 2340
Dh 2280 AGGTGCGAGAAAAACATTTGCAAAATTTGTTTCTTCCAGAAATTCAGAAAACT 2339
Qy 2341 TGGTCAAAAAATACCCCAATTAATGTCTTTTGAAGATTTTCATTAATAACACAGAA 2400
Dh 2340 TGGTCAAAAAATACCCCAATTAATGTCTTTTGAAGATTTTCATTAATAACACAGAA 2399
Qy 2401 TTTTGAATCCCGGATGTAATTTTGTGTAATTAATTAATTAATTAATTAATTAAT 2460
Dh 2400 TTTTGAATCCCGGATGTAATTTTGTGTAATTAATTAATTAATTAATTAATTAAT 2459
Qy 2461 ATTAATAAGTTATTTTCTATTCGAAATTTTAAAGCATTTTTCCTGATTTGATTT 2520
Dh 2460 ATTAATAAGTTATTTTCTATTCGAAATTTTAAAGCATTTTTCCTGATTTGATTT 2519
Qy 2521 GCGAAAAAGATCTGATTTTCAAAAAATCGGTTTTTAAATGTAATTTTGGAAAAAT 2580
Dh 2520 GCGAAAAAGATCTGATTTTCAAAAAATCGGTTTTTAAATGTAATTTTGGAAAAAT 2579
Qy 2581 ACATTAATAATGATTTTGAATTTTGAATTTTCTTTCGAAAAACAGTTTCTGCTGATTCG 2640
Dh 2580 ACATTAATAATGATTTTGAATTTTGAATTTTCTTTCGAAAAACAGTTTCTGCTGATTCG 2639
Qy 2641 TGAACGAAAAACCCCAAAATTCATTTTCAAAATTAATAACCAAGAAAAATCGTTTTT 2700
Dh 2640 TGAACGAAAAACCCCAAAATTCATTTTCAAAATTAATAACCAAGAAAAATCGTTTTT 2699
Qy 2701 TAACTTAATTTTCCGCGCAAGAAATGAAGCAATTAATTAATTAATTAATTAAT 2760
Dh 2700 TAACTTAATTTTCCGCGCAAGAAATGAAGCAATTAATTAATTAATTAATTAAT 2759
Qy 2761 GGTCTAATCTGTTGGCGGTTTCTGATGCAAAAAATGATGGAATCCGTGGAACCTGAG 2820
Dh 2760 GGTCTAATCTGTTGGCGGTTTCTGATGCAAAAAATGATGGAATCCGTGGAACCTGAG 2819
Qy 2821 GGAAGATGCGAAACCTCTTCTTACACATGCTGTTCAATAAAGCGGATCCGCAAC 2880
Dh 2820 GGAAGATGCGAAACCTCTTCTTACACATGCTGTTCAATAAAGCGGATCCGCAAC 2879
Qy 2881 AACTGGAAGAACACAAATCGAGCTGGATTAAGAGATTTTGCATAGACATTAAGAATCAA 2940
Dh 2880 AACTGGAAGAACACAAATCGAGCTGGATTAAGAGATTTTGCATAGACATTAAGAATCAA 2939
Qy 2941 TATCCCTTTTCCCTAGTACCTTGAATTTCCGCGGCTGTGTAAAGCCGATTAATACAG 3000
Dh 2940 TATCCCTTTTCCCTAGTACCTTGAATTTCCGCGGCTGTGTAAAGCCGATTAATACAG 2999
Qy 3001 GTTGGATGCTCTTGGGGGAGACAGTGAACATTAATCAATTAATTAATTAATTAAT 3060
Dh 3000 GTTGGATGCTCTTGGGGGAGACAGTGAACATTAATCAATTAATTAATTAATTAAT 3059
Qy 3061 AATGTTATTTGTTACGGGAATFACAAAAATTCGAGAAATGCTATTTCAACATATTTGAGCG 3120
Dh 3060 AATGTTATTTGTTACGGGAATFACAAAAATTCGAGAAATGCTATTTCAACATATTTGAGCG 3119
Qy 3121 GCAAAATATCCAGTGAAGAAATCAAGATTAATTTTAAATTTTAAATTTTAAATTT 3180
Dh 3120 GCAAAATATCCAGTGAAGAAATCAAGATTAATTTTAAATTTTAAATTTTAAATTT 3179

QY	3181	AAANAANAATACCACTPAATCAAAAGAAATTAATTTCAAAAAATCGAGCCCGTAATCGACT	3240
Dp	3180	AAAAAANAATACCACTPAATCAAAAGAAATTAATTTCAAAAAATCGAGCCCGTAATCGACT	3239
QY	3241	ACACTAGCACTTTAAAGAAATTAAGTATGTTTTCGCTACAGAGATTAATTTCCGCTCAAAATAT	3300
Dp	3240	ACACTAGCACTTTAAAGAAATTAAGTATGTTTTCGCTACAGAGATTAATTTCCGCTCAAAATAT	3299
QY	3301	GTGTGAAATTAAGCATTCACGAGATTTTGTGTCCCGGAATATGCTCTAAAGCATTAAT	3360
Dp	3300	GTGTGAAATTAAGCATTCACGAGATTTTGTGTCCCGGAATATGCTCTAAAGCATTAAT	3359
QY	3361	TGTGAAANAATTAANAATTCAGAAAAAATTTGCGAGAGACACTTATGACACTCGGAAAAACA	3420
Dp	3360	TGTGAAANAATTAANAATTCAGAAAAAATTTGCGAGAGACACTTATGACACTCGGAAAAACA	3419
QY	3421	ATGAAGAAGAGACTACGAGACAGAGAGAGTGAAAAAAGTGGAGCGCGGAGAGAGACAGACA	3480
Dp	3420	ATGAAGAAGAGACTACGAGACAGAGAGAGTGAAAAAAGTGGAGCGCGGAGAGAGACAGACA	3479
QY	3481	CGGTGTGATGATTTGGCGCTGAGTACAGCTGAGACCCATTGGAATCGTTGGAGTGTG	3540
Dp	3480	CGGTGTGATGATTTGGCGCTGAGTACAGCTGAGAGCCATTGGAATCGTTGGAGTGTG	3539
QY	3541	GTGTGTGGGGGAGTGAAGTTCACCTGAGTGAACGATATTCATTTGTGTAATAATTAAT	3600
Dp	3540	GTGTGTGGGGGAGTGAAGTTCACCTGAGTGAACGATATTCATTTGTGTAATAATTAAT	3599
QY	3601	TTATGTACAACTCCCTTCATTTGAATCTCATTTTTCCTACAGATTCCTATCCCTTGA	3660
Dp	3600	TTATGTACAACTCCCTTCATTTGAATCTCATTTTTCCTACAGATTCCTATCCCTTGA	3659
QY	3661	ACTGGAAGAAAGTGGAAAGCTAGGCCACAATTAACGGCTCTGTGTGCGATTTACAGATTT	3720
Dp	3660	ACTGGAAGAAAGTGGAAAGCTAGGCCACAATTAACGGCTCTGTGTGCGATTTACAGATTT	3719
QY	3721	TACGCAATTTTTCGATGCGCTTTTTTTGGCCAAACCTACTCCGGTAAATATACA	3780
Dp	3720	TACGCAATTTTTCGATGCGCTTTTTCGTTTGGCCAAACCTACTCCGGTAAATATACA	3779
QY	3781	ACTTTCCGCTGTCTGACATTTTCGTCAAAAACCCGAAACCCTAATTTCTCGCGCTG	3840
Dp	3780	ACTTTCCGCTGTCTGACATTTTCGTCAAAAACCCGAAACCCCTAATTTCTCGCGCTG	3839
QY	3841	GCCTAGCCCTCCGCTCTCTCCACATTTCCAAAGTACCCGTATTCATTAATTTATTC	3900
Dp	3840	GCCTAGCCCTCCGCTCTCTCCACATTTCCAAAGTACCCGTATTCATTAATTTATTC	3899
QY	3901	TTTCCTTAATCTGTCTCTTTCGTGTGGGCTCTCCAACTCCCCCAAAATTTCTGTAGCG	3960
Dp	3900	TTTCCTTAATCTGTCTCTTTCGTGTGGGCTCTCCAACTCCCCCAAAATTTCTGTAGCG	3959
QY	3961	GTAGCGCACTTGTATTAATTTTTCCAAAATTTTCTCTCTACACACAAAAAATTAAC	4020
Dp	3960	GTAGCGCACTTGTATTAATTTTTCCAAAATTTTCTCTCTACACACAAAAAATTAAC	4019
QY	4021	GGTCTTTTATTCACCCCTTTTTCGGAACGAAATGCAATTTTGATATAAGCGCTGGC	4080
Dp	4020	GGTCTTTTATTCACCCCTTTTTCGGAACGAAATGCAATTTTGATATAAGCGCTGGC	4079
QY	4081	AAGAGAAATCGGTTTTCATTTTGGCCATCAGCTATCCAAAAAATTTAGTAGAGAAATA	4140
Dp	4080	AAGAGAAATCGGTTTTCATTTTGGCCATCAGCTATCCAAAAAATTTAGTAGAGAAATA	4139
QY	4141	TCAATTTTATATAATGATTCATCTTTCGCGCTCTTCTGTCTGAGAGCAGCGCTCAT	4200
Dp	4140	TCAATTTTATATAATGATTCATCTTTCGCGCTCTTCTGTCTGAGAGCAGCGCTCAT	4199
QY	4201	TGCAATGCGCTGAATTTTTCGAAAAAANAATTTTGTTAGTGTAAACGATCCCCC	4260
Dp	4200	TGCAATGCGCTGAATTTTTCGAAAAAANAATTTTGTTAGTGTAAACGATCCCCC	4259
QY	4261	GCCTTATTCGCTGTTTCACATTCAGATAGGCTCGCCATTGATTCCTTGAATTTTGTG	4320

Db	4260	GCCTTATGCGTGTTCACCAATCAGATRAGGCTCCGCCATTTGATTCCTTGAATTTTGCG	4319
Qy	4321	GTAATATAAACCAAAAACGTTAGTGCAGATTCGAAAAACAATGCGTCTTACTAT	4380
Db	4320	GTAATATAAACCAAAAACGTTAGTGCAGATTCGAAAAACAATGCGTCTTACTAT	4379
Qy	4381	TCACCTCTGTTGTTCTTTTGCGTTTGCGCTTTTGTTGTGAGCAAGAAGACATCTACTG	4440
Db	4380	TCACCTCTGTTGTTCTTTTGCGCTTTTGTTGTGAGCAAGAAGACATCTACTG	4439
Qy	4441	TCACAGGTCACACTAATTTGTATATAGAAGAAATTCAGGMRAGTTACCTTTGGAGAA	4500
Db	4440	TCACAGGTCACACTAATTTGTATATAGAAGAAATTCAGGMRAGTTACCTTTGGAGAA	4499
Qy	4501	AGATACCTGAGGTTTTCACTCTTGTGTTAGCTTGAACGGCTTAAAAAGACTAAAAAG	4560
Db	4500	AGATACCTGAGGTTTTCACTCTTGTGTTAGCTTGAACGGCTTAAAAAGACTAAAAAG	4559
Qy	4561	CCTAAAAATTGAAGTTTCCACCTGTTTCTAAAAAGAACCGAATTCGACAGCTTTAC	4620
Db	4560	CCTAAAAATTGAAGTTTCCACCTGTTTCTAAAAAGAACCGAATTCGACAGCTTTAC	4619
Qy	4621	GAGATTCTCATATATTGTATTTGAATTTTCATATTCATCCCAACAGTCTCTTAC	4680
Db	4620	GAGATTCTCATATATTGTATTTGAATTTTCATATTCATCCCAACAGTCTTTAC	4679
Qy	4681	GAATTTTGCAATTTTGTAGCTTAAAAATACGATACCTGTGTCGACAGAAACATTTTG	4740
Db	4680	GAATTTTGCAATTTTGTAGCTTAAAAATACGATACCTGTGTCGACAGAAACATTTTG	4739
Qy	4741	TTAAATTTCAAAAAGATGCGGCTTTAAAGAGTCGTAGTTGAACTCTGTTGTTC	4800
Db	4740	TTAAATTTCAAAAAGATGCGGCTTTAAAGAGTCGTAGTTGAACTCTGTTGTTC	4799
Qy	4801	GGACCTTTCATCGATTTTGTGTAGCGTTTATATAGAAAAATGTATTTATTTATCA	4860
Db	4800	GGACCTTTCATCGATTTTGTGTAGCGTTTATATAGAAAAATGTATTTATTTATCA	4859
Qy	4861	AAATTTAATTTTACCGATCGCGAAAAACAATGAAGAACCGATAAAAATATCGAG	4920
Db	4860	AAATTTAATTTTACCGATCGCGAAAAACAATGAAGAACCGATAAAAATATCGAG	4919
Qy	4921	CACACATATGTTGAAATTTACAGTCTCTTTAAGGNNNCATTTCCATATTTCCAC	4980
Db	4920	CACACATATGTTGAAATTTACAGTCTCTTTAAGGNNNCATTTCCATATTTCCAC	4979
Qy	4981	AAACCTTGTCGTGTGNNNCGGATCGTCAATTTATGTCAGAAAAATTCGAT	5040
Db	4980	AAACCTTGTCGTGTGNNNCGGATCGTCAATTTATGTCAGAAAAATTCGAT	5039
Qy	5041	ATATGTTCAAAAAACCACAATATATGCGAATTTCAAGCTTGAAGCGAAATTCAGAAAT	5100
Db	5040	ATATGTTCAAAAAACCACAATATATGCGAATTTCAAGCTTGAAGCGAAATTCAGAAAT	5099
Qy	5101	TCTAAAAATTAAAAAAATCATTTCCGAATGTGAATTTGTGATTTTCACCTGAGTCCAT	5160
Db	5100	TCTAAAAATTAAAAAAATCATTTCCGAATGTGAATTTGTGATTTTCACCTGAGTCCAT	5159
Qy	5161	ATGGCAAAATTCGTCATATTCGNNNTTCGANNATTTGTTTCCACGTCGGCGGAAAAAG	5220
Db	5160	ATGGCAAAATTCGTCATATTCGNNNTTCGANNATTTGTTTCCACGTCGGCGGAAAAAG	5219
Qy	5221	AAAGCAGCAANNACTGATTTGCGCAATTTTTCCTGACGTCGTCAATTTATTTGAATC	5280
Db	5220	AAAGCAGCAANNACTGATTTGCGCAATTTTTCCTGACGTCGTCAATTTATTTGAATC	5279
Qy	5281	TATATAGCTGTATTTTCTGCTATTTGACAACTAAGTGAATCATATATTTGCAATTTAA	5340
Db	5280	TATATAGCTGTATTTTCTGCTATTTGACAACTAAGTGAATCATATATTTGCAATTTAA	5339
Qy	5341	TATTACCTTTGATGTGGCTTAGAAAAAAACCACAAAACCTCATCTAGCTTAGGC	5400

Db 5340 TATTGACTTTTGATGTGTGGCTTGAAGAAAAAACCCTATCTAGCTTTAGGC 5399
 QY 5401 TGCCAAATATATTCCTAGACATATAAACCCTTTAAATTCCTGCAACACCTACAGC 5460
 Db 5400 TGCCAAATATATTCCTAGACATATAAACCCTTTAAATTCCTGCAACACCTACAGC 5459
 QY 5461 TATCAACGACTATTAATTAATTCATTCGACCCGCAATGCAAGCTCCCTCA 5520
 Db 5460 TATCAACGACTATTAATTAATTCGATTCGACCCGCAATGCAAGCTCCCTCA 5519
 QY 5521 TGCATGCAACAAAGAGAGAGTCTCACTTACCGGATCCGACGACGATCACCCTCA 5580
 Db 5520 TGCATGCAACAAAGAGAGAGTCTCACTTACCGGATCCGACGACGATCACCCTCA 5579
 QY 5581 TCTCTCCATACCTCATATACCCACCACTGCAAGTGAAGAGCCGATGCAAGCTG 5640
 Db 5580 TCTCTCCATACCTCATATACCCACCACTGCAAGTGAAGAGCCGATGCAAGCTG 5639
 QY 5641 TTTCAAGATTTGATTTCCAAAGAGAGTGGTGAACCTATGATATGACATACGTC 5700
 Db 5640 TTTCAAGATTTGATTTCCAAAGAGAGTGGTGAACCTATGATATGACATACGTC 5699
 QY 5701 CTCTTGATATTCCTCCGCTAAGACAGAGAGAGTCTTAAGAAATGTTTTTGT 5760
 Db 5700 CTCTTGATATTCCTCCGCTAAGACAGAGAGTCTTAAGAAATGTTTTTGT 5759
 QY 5761 GGTTCCTGTTGTTGAAGAGAGACTTCTATCTCTTTTAAATCAATTAACATAT 5820
 Db 5760 GGTTCCTGTTGTTGAAGAGAGACTTCTATCTCTTTTAAATCAATTAACATAT 5819
 QY 5821 GAAACCGTGAATTTTAACTTGAACGTAAGAAAAAGTTGGCTATTAATGTTGCAAT 5880
 Db 5820 GAAACCGTGAATTTTAACTTGAACGTAAGAAAAAGTTGGCTATTAATGTTGCAAT 5879
 QY 5881 TTTGGCAAGTATCTTTGTTGATATCAATTAACGATCAAGAGAGAAATTAAG 5940
 Db 5880 TTTGGCAAGTATCTTTGTTGATATCAATTAACGATCAAGAGAGAAATTAAG 5939
 QY 5941 GAAACAGAAATTAATGAGATGGCAACATTTGACCGCAAAATATCTGTAAGCA 6000
 Db 5940 GAAACAGAAATTAATGAGATGGCAACATTTGACCGCAAAATATCTGTAAGCA 5999
 QY 6001 CTACAGTATTTCTCAAAAGACTAGTGTAGCGCTGTGTGATTTAGAGCTGATTTTG 6060
 Db 6000 CTACAGTATTTCTCAAAAGACTAGTGTAGCGCTGTGTGATTTAGAGCTGATTTTG 6059
 QY 6061 AAATGATCAGACTAGAGAGAGAGAGAAATTTGAACATCAATGAAATCAATCA 6120
 Db 6060 AAATGATCAGACTAGAGAGAGAGAGAAATTTGAACATCAATGAAATCAATCA 6119
 QY 6121 AAAAGTCGAACCTTACAGTACAGTGTCTTAAGAAATTAAGTGTGTGTGTGTG 6180
 Db 6120 AAAAGTCGAACCTTACAGTACAGTGTCTTAAGAAATTAAGTGTGTGTGTGTG 6179
 QY 6181 ATATTTTGGNGNGCAAAATGTTGNGCAATACGCAATCTCTCAATTTGTGTGTGT 6240
 Db 6180 ATATTTTGGNGNGCAAAATGTTGNGCAATACGCAATCTCTCAATTTGTGTGTGT 6239
 QY 6241 TGTCTTGAATTTTCCATTTCAACATCAATTAAGCAAAATGTTGTGTGTGTG 6300
 Db 6240 TGTCTTGAATTTTCCATTTCAACATCAATTAAGCAAAATGTTGTGTGTGTG 6299
 QY 6301 GCGACACATGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6360
 Db 6300 GCGACACATGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6359
 QY 6361 CAATATCAATTTTAAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6420
 Db 6360 CAATATCAATTTTAAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6419
 QY 6421 TTTGAGTGCAGAACTTATTAATTCGCGGCTCTCAAAAGTCTTTTGTGAAA 6480
 Db 6420 TTTGAGTGCAGAACTTATTAATTCGCGGCTCTCAAAAGTCTTTTGTGAAA 6479

QY 6481 TATAAGCTTTATATATTTATATTTAAATTTGATTCATGATATCAAAAGGACTA 6540
 Db 6480 TATAAGCTTTATATATTTATATTTAAATTTGATTCATGATATCAAAAGGACTA 6539
 QY 6541 GTTTGATTAATAATTTATCA 6560
 Db 6540 GTTTGATTAATAATTTATCA 6559

RESULT 5
 US-60-360-039-29563
 ; Sequence 29563, Application US/60360039
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Chen, Xianfeng
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)A
 ; CURRENT FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 29563
 ; LENGTH: 713
 ; TYPE: DNA
 ; ORGANISM: Caenorhabditis elegans
 US-60-360-039-29563

Query Match 10.9%; Score 713; DB 80; Length 713;
 Best Local Similarity 100.0%; Pred No. 1.1e-103;
 Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 772 ATGATTAACATCCAACTGCGATTTCTGTGCGGCTTGGGCGCAGATCTGATTTCCGCG 831
 Db 1 ATGATTAACATCCAACTGCGATTTCTGTGCGGCTTGGGCGCAGATCTGATTTCCGCG 830
 QY 832 TCCTTTGGAACATCGATCGTCCACCAAGTGGGGATTTTGAATTTTCCGTAATTTG 891
 Db 61 TCCTTTGGAACATCGATCGTCCACCAAGTGGGGATTTTGAATTTTCCGTAATTTG 890
 QY 892 TTGATTTTGTGTAGCATGAAGCAAAATGATTAACAGACATCTTTCAATTAAT 951
 Db 121 TTGATTTTGTGTAGCATGAAGCAAAATGATTAACAGACATCTTTCAATTAAT 950
 QY 952 TATTTAATATTTACAGTCCGAGCAAGAGCCAAATCCGAAGTTGGATGGAATAC 1011
 Db 181 TATTTAATATTTACAGTCCGAGCAAGAGCCAAATCCGAAGTTGGATGGAATAC 1010
 QY 1012 CTGTGTAACGACGCTCCCAAGATGCCCAATGCGTCCCATCTCACGCTGTACAGCA 1071
 Db 241 CTGTGTAACGACGCTCCCAAGATGCCCAATGCGTCCCATCTCACGCTGTACAGCA 1070
 QY 1072 CAATGACCTGATGCTCTCGGATTTCCATGAATACAGCGGTGTGTAAATGCGGAAAC 1131
 Db 301 CAATGACCTGATGCTCTCGGATTTCCATGAATACAGCGGTGTGTAAATGCGGAAAC 1130
 QY 1132 CTTCGCTGCGAGGATGGAATGCGATTTGCGGCTTGCATTTACCGCTTTTGTGAT 1191
 Db 361 CTTCGCTGCGAGGATGGAATGCGATTTGCGGCTTGCATTTACCGCTTTTGTGAT 1190
 QY 1192 TTTATCCCTAGCTGGAATTTACATGCGGCGTGAACCGCTCTCTTCAAGTATCATATGCT 1251
 Db 421 TTTATCCCTAGCTGGAATTTACATGCGGCGTGAACCGCTCTCTTCAAGTATCATATGCT 1250
 QY 1252 TTCCCATCATTTTCCATCTCTTAACGGAATTCGCTTTAGATTCATTTGGCTAAG 1311
 Db 481 TTCCCATCATTTTCCATCTCTTAACGGAATTCGCTTTAGATTCATTTGGCTAAG 1310
 QY 1312 GGAATCAATATGTTGAGACAGTAGAGTGAATTAATTAATTTTAAATTA 1371
 Db 1312 GGAATCAATATGTTGAGACAGTAGAGTGAATTAATTAATTTTAAATTA 1370

LENGTH: 1315 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 7..846
OTHER INFORMATION: /product= "Ced-9"

Query Match

Best Local Similarity 9.6%; Score 632.6; DB 6; Length 1315;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3393 GGAAGCTTATGATGACATGCGAAACAAATGAAAGGAGCTACAGAGAGAGAGAGCTGA 3452
DB 669 GGAGCACTTATGATGACATGCGAAACAAATGAAAGGAGCTACAGAGAGAGAGAGCTGA 728
QY 3453 AAAAGTGGAGCGCGGAG 3512
DB 729 AAAAGTGGAGCGCGGAG 788
QY 3513 TGGAGCATTGGAATGTTGGAGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 3572
DB 789 TGGAGCATTGGAATGTTGGAGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 848
QY 3573 AGCTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3632
DB 849 AGCTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 908
QY 3633 TTGGCTACTGATTCCTCATCTTTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 3692
DB 909 TTGGCTACTGATTCCTCATCTTTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 968
QY 3693 TAGGCTCTGTGTGATTTAGATTTTACATTTTTCGATTTTTCGATTTTTCGATTTT 3752
DB 969 TAGGCTCTGTGTGATTTAGATTTTACATTTTTCGATTTTTCGATTTTTCGATTTT 1028
QY 3753 GGCCAAACCTTACCTGCGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3812
DB 1029 GGCCAAACCTTACCTGCGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1088
QY 3813 CCCTGAACCTTACCTGCGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3872
DB 1089 CCCTGAACCTTACCTGCGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1148
QY 3873 AAGTACCCCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3932
DB 1149 AAGTACCCCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1208
QY 3933 TTCCAACTCCCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3992
DB 1209 TTCCAACTCCCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1268
QY 3993 GTTTTCTCTCTACACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAT 4025
DB 1269 GTTTTCTCTCTACACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAT 1301

RESULT 8

US-08-288-295-4
Sequence 4, Application US/08288295
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Hengartner, Michael
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: FISH & RICHARDSON
STREET: 225 Franklin Street, Suite 3100

CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A. (F) ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,295
FILING DATE: 10-AUG-1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/927,681
FILING DATE: 10-AUG-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 01997/201003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1315 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 7..846
OTHER INFORMATION: /product= "Ced-9"

Query Match

Best Local Similarity 9.6%; Score 632.6; DB 6; Length 1315;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3393 GGAAGCTTATGATGACATGCGAAACAAATGAAAGGAGAGCTACAGAGAGAGAGAGCTGA 3452
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QY 3453 AAAAGTGGAGCGCGGAG 3512
DB 729 AAAAGTGGAGCGCGGAG 788
QY 3513 TGGAGCATTGGAATGTTGGAGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 3572
DB 789 TGGAGCATTGGAATGTTGGAGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 848
QY 3573 AGCTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3632
DB 849 AGCTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 908
QY 3633 TTGGCTACTGATTCCTCATCTTTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 3692
DB 909 TTGGCTACTGATTCCTCATCTTTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 968
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DB 969 TAGGCTCTGTGTGATTTAGATTTTACATTTTTCGATTTTTCGATTTTTCGATTTT 1028
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DB 1029 GGCCAAACCTTACCTGCGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1088
QY 3813 CCCTGAACCTTACCTGCGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3872
DB 1089 CCCTGAACCTTACCTGCGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1148

TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELE: 200154
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1315 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..846
 OTHER INFORMATION: /product= "Ced-9"

Query Match 9.6%; Score 632.6; DB 6; Length 1315;
 Best Local Similarity 99.8%; Pred. No. 8e-91;
 Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3393 GGACGACTTATGACACTCGGAAACAAATGAAAGAGACTACGAGAGAGAGAGCTGA 3452
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 DB 729 AAAAGTGGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 788
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 DB 849 ACATATTCATTTGTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
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 DB 969 TACGGCTCTGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 1028
 QY 3753 GGCCAAACCCCTACTCCGCGTAATATCACTTTCCGCTTCGTAATTTTCTGCAAAA 3812
 DB 1029 GGCCAAACCCCTACTCCGCGTAATATCACTTTCCGCTTCGTAATTTTCTGCAAAA 1088
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 DB 1269 GTTTTCTCTACACAAACAAAAAGGCTTC 1301

RESULT 11
 ; Sequence 2, Application us/08801248
 ; GENERAL INFORMATION:
 ; APPLICANT: Horvitz, H. Robert
 ; APPLICANT: Hengartner, Michael
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 ; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED

TITLE OF INVENTION: CELL DEATH AND USES THEREFOR
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & RICHARDSON
 STREET: 225 Franklin Street, Suite 3100
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,248
 FILING DATE: 19-FEB-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/288,295
 FILING DATE: 10-AUG-1994
 APPLICATION NUMBER: US 07/927,681
 FILING DATE: 10-AUG-1992
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 01997/201003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1315 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..846
 OTHER INFORMATION: /product= "Ced-9"

Query Match 9.6%; Score 632.6; DB 12; Length 1315;
 Best Local Similarity 99.8%; Pred. No. 8e-91;
 Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3393 GGACGACTTATGACACTCGGAAACAAATGAAAGAGAGACTACGAGAGAGAGAGCTGA 3452
 DB 669 GGACGACTTATGACACTCGGAAACAAATGAAAGAGAGACTACGAGAGAGAGAGCTGA 728
 QY 3453 AAAAGTGGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3512
 DB 729 AAAAGTGGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 788
 QY 3513 TGGAGCCATTGGAATGTTGGAGTGTGCTGTGGGCGGATGATGCTTGAAGTA 3572
 DB 789 TGGAGCCATTGGAATGTTGGAGTGTGCTGTGGGCGGATGATGCTTGAAGTA 848
 QY 3573 ACATATTCATTTGTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3632
 DB 849 ACATATTCATTTGTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
 QY 3633 TTTGCTACTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 3692
 DB 909 TTKGCTCACTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 968
 QY 3693 TACGGCTCTGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 3752
 DB 969 TACGGCTCTGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 1028

US-08-801-248-4

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CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/801,248
 FILING DATE: 19-FEB-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/288,295
 FILING DATE: 10-AUG-1994
 APPLICATION NUMBER: US 07/927,681
 FILING DATE: 10-AUG-1992
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 01997/201003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1315 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..846
 OTHER INFORMATION: /product= "Ced-9"
 US-08-801-248-5

Query Match
 Best Local Similarity 9.6%; Score 632.6; DB 12; Length 1315;
 Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

3393 GGACGACTTCTGACACCTCGGAAACAAATGAAGAGAGCTACGAACGAGCAGACCTGA 3452
 669 GGAGGACTTCTGACACCTCGGAAACAAATGAAGAGAGCTACGAACGAGCAGACCTGA 728
 3453 AAAAGTGGAGCGCCGGAAGACAGACGCGTGTGATGATGGCGCTGGAGTAACAGC 3512
 729 AAAAGTGGAGCGCCGGAAGACAGACGCGTGTGATGATGGCGCTGGAGTAACAGC 788
 3513 TGGAGCATTGGAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3572
 789 TGGAGCATTGGAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 848
 3573 ACCTATTCATTTGTGTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3632
 849 ACCTATTCATTTGTGTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
 3633 TTGGCTCAGTATTCCTGATCTTTGAACGGAAGAGTGGAAAGCTAGCCACAAT 3692
 909 TTGGCTCAGTATTCCTGATCTTTGAACGGAAGAGTGGAAAGCTAGCCACAAT 968
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 969 TACGGCTCTGTGTCGATTTACGATTTTACGATTTTCCGATTTTCCGATTTTCCGATTTTCCGAT 1028
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 1209 TTCCAACTCCCGCAAAATTCCTAGCGTACGCGACTTTGATTAATTTTCAAAAT 1268

3993 GTTTCCTCTACACAAACAAACAAACGCTG 4025
 1269 GTTTCCTCTACACAAACAAACAAACGCTG 1301

RESULT 14

US-08-801-248-6
 Sequence 6, Application US/08801248
 GENERAL INFORMATION:
 APPLICANT: Horvitz, H. Robert
 TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & RICHARDSON
 STREET: 225 Franklin Street, Suite 3100
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,248
 FILING DATE: 19-FEB-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/288,295
 FILING DATE: 10-AUG-1994
 APPLICATION NUMBER: US 07/927,681
 FILING DATE: 10-AUG-1992
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 01997/201003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1315 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..846
 OTHER INFORMATION: /product= "Ced-9"
 US-08-801-248-6

Query Match
 Best Local Similarity 9.6%; Score 632.6; DB 12; Length 1315;
 Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

3393 GGACGACTTCTGACACCTCGGAAACAAATGAAGAGAGCTACGAACGAGCAGACCTGA 3452
 669 GGAGGACTTCTGACACCTCGGAAACAAATGAAGAGAGCTACGAACGAGCAGACCTGA 728
 3453 AAAAGTGGAGCGCCGGAAGACAGACGCGTGTGATGATGGCGCTGGAGTAACAGC 3512
 729 AAAAGTGGAGCGCCGGAAGACAGACGCGTGTGATGATGGCGCTGGAGTAACAGC 788
 3513 TGGAGCATTGGAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3572

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us-09-993-420a-1.rtf

Page 22

Db	789	TGGAGCCATTGGAAATCGTGTGAGTCGTGCTGTGTGGCGGAGATGATGTTCCACCTGGAACTA	848
Qy	3573	ACGATATCAATTTGGTAATAATTAATTTATGTACAACCTCTTACATTTGAACATCTCATTT	3632
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Db	909	TTTGGCTACATGATTTCTGCATACCTTTGAACGTGGAGAAAGTGGAAAGCTTAGGCCACAAT	968
Qy	3693	TACGGCTCTGTGTGCGATTTACGATTTTACTGCAATTTTTTCCGATTCGCTTTT	3752
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Qy	3813	CCCTGAACCCCTAACTTTTCTGCGCGTGGCCCTAGCCCTCCCGGCTTCCTTCCACATTTTCCA	3872
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Qy	3873	AATTAACCCCTGTATCTCAATATATTCATCTTCACCTTTTAACTGTCTCTTTTGTGTGGGCTC	3932
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Db	1209	TTTCCAACTCCCGCAAAATTCCTGTAGCGGTAAAGGACCTTGTATTTATTTTTCAAAT	1268
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RESULT 15
US-09-993-420A-2
: Sequence 2, Application US/09993420A

1 GENEABSTRACT
 2 APPLICANT: Horvitz, H. Robert
 3 APPLICANT: Hengartner, Michael
 4 TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 5 TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
 6 TITLE OF INVENTION: USES THEREOF
 7 FILE REFERENCE: 01997/201006
 8 CURRENT APPLICATION NUMBER: US/09/993,420A

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? FILE REFERENCE: APPLICATION NUMBER: US/09/993,420A
? CURRENT FILING DATE: 5001-11-09
? PRIOR APPLICATION NUMBER: 09/234,166
? PRIOR FILING DATE: 1999-01-20
? PRIOR APPLICATION NUMBER: 07/898,933
? PRIOR FILING DATE: 1992-06-12
? PRIOR APPLICATION NUMBER: 07/927,681
? PRIOR FILING DATE: 1992-08-10
? PRIOR APPLICATION NUMBER: 08/288,295
? PRIOR FILING DATE: 1994-08-10
? PRIOR APPLICATION NUMBER: 08/801,248
? PRIOR FILING DATE: 1997-02-19
? NUMBER OF SEQ ID NOS: 8
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 2
? LENGTH: 1315
? TYPE: DNA
? ORGANISM: Caenorhabditis elegans
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (7)...(846)
US-09-993-420A-2

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Query Match	9.6%	Score 632.6;	DB 37;	Length 1315;
Best Local Similarity	99.8%;	Pred. No. 8e-91;		
Matches 632; Conservative	1;	Mismatches	0;	Gaps 0
QY	3393	GGAGCACTTCATGACACTCGGAAAAACAATGAAGAGACTTCGACAGAGAGAGAGCTGA	3452	

[illegible]

Search completed: February 28, 2003, 08:42:54
Job time : 12517.6 secs

XX Caenorhabditis elegans cell death-protective gene - used to
PT develop agents for preventing cell death or for reducing
PT population of cells
XX
PS Claim 3; Page 54-58; 112pp; English.
XX
CC ced-9 is essential for C. elegans development and apparently
CC functions by protecting cells during development from programmed
CC cell death. ced-9 was shown to function by antagonising the
CC activities of cell death genes ced-3 and ced-4. The protein product
CC of the human oncogene bcl-2 was found to have a similar sequence
CC to the ced-9 protein. The ced-9 gene can be used for developing
CC agents for treating a condition characterised by increased cell death
CC such as myocardial infarction, stroke, traumatic brain injury,
CC neurodegenerative disease, muscular degenerative disease, ageing,
CC hypoxia, ischaemia, toxemia, infection or hair loss. It can also
CC be used for reducing a population of cells in the treatment of
CC neoplastic growth cancersous tissue, infected cells or autoreactive
CC immune cells.
XX
SQ Sequence 6560 BP; 2040 A; 1274 C; 1203 G; 2023 T; 20 other:
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 6556; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 1921 ATTATGAAAAATCAATGATGAGGAGAGCAGCAGCTTGATATCAGAGGATTTGGTA 1920
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QY 1981 CACCGAATCCGCAAAAACGAAATGGAATGTTGAGACCGGGAGTTCCGCTGAGAGT 2040
| | | | |
Db 1981 CACCGAATCCGCAAAAACGAAATGGAATGGAATGTTGAGACCGGGAGTTCCGCTGAGAGT 2040
| | | | |
QY 2041 CACCGGAGAGCAATGATGAGCAGTATGGAACGATATTCGAGAGAGCAGCGGAA 2100
| | | | |
Db 2041 CACCGGAGAGCAATGATGAGCAGTATGGAACGATATTCGAGAGAGCAGCGGAA 2100
| | | | |
QY 2101 AATTTGAGACCTTCTGTAGCAGCTCGCAGTGGCCAGAACTCATTTTCACCTGAT 2160
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QY 2161 CAGGATGCTGCGAGCAGCTTGAAATGACAGACAGATCAATGTCATGCTTATGA 2220
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Db 2161 CAGGATGCTGCGAGCAGCTTGAAATGACAGACAGATCAATGTCATGCTTATGA 2220
| | | | |
QY 2221 CGTTGTAAGGAGAAATCTGAAAAAAGTTGCAAAAATTCGAAAAATTCGCCGAA 2280
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| | | | |
Db 2281 AGTGGCAGAAAAAATCATTTGCAAAAATGTTGTTCTCTCGAGAAATCAGCAAAATC 2340
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| | | | |
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| | | | |
QY 2461 ATTAAAAACGTTATTTCTATTCGAATATTTTAAAGCAATTTTCTGATTTGATTT 2520
| | | | |
Db 2461 ATTAAAAACGTTATTTCTATTCGAATATTTTAAAGCAATTTTCTGATTTGATTT 2520
| | | | |
QY 2521 GCGAAAAAGATGCTGATTTATCAAAAATCGGTTTAAATGTAATTTTGTGAAAT 2580
| | | | |
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| | | | |
QY 2581 ACATTAATTCGATTTTGAATTTTCTCTCGAAAAACAGGTTTCTGATTTG 2640
| | | | |
Db 2581 ACATTAATTCGATTTTGAATTTTCTCTCGAAAAACAGGTTTCTGATTTG 2640
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Db 2641 TGAACGAAAAACCCCAAAATTCATTTTGAACATTTAAAAACCGAAAAATTCGTTTTT 2700
| | | | |
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| | | | |
Db 2701 TAAGCTTAATTTTCCGCGGAAATGAGCAATTAATTTGCAATTTCTAATTTTCAGATA 2760
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QY 2761 GGTCTAATCTGCTGGGGGTTTCGTAGCTGCAAAAATGATGAGATCCGTTGAGAGT 2820
| | | | |
Db 2761 GGTCTAATCTGCTGGGGGTTTCGTAGCTGCAAAAATGATGAGATCCGTTGAGAGT 2820
| | | | |
QY 2821 GGACAAGTGCAGAACTCTGCTGTTACAGATCGCTGTTCAAAAACGCGGATCCGCAAC 2880
| | | | |
Db 2821 GGACAAGTGCAGAACTCTGCTGTTACAGATCGCTGTTCAAAAACGCGGATCCGCAAC 2880
| | | | |

QY 2881 AACTGGAAGGAGACATTCGAGAGTGGGTTAGAGATTTTGCATAGACATTTAGAGTCAA 2940
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| | | | |
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| | | | |
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| | | | |
QY 3121 GCAAAATATCCAGTACAGAAAATCAGTAATCTTTTAAATTTTAAATTTTACAAAT 3180
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| | | | |
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QY 3301 GTTGAATATCCGCTACGAGATTTTGTGTTTCCCGGAAATATGCTTAACATTAAT 3360
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Db 3301 GTTGAATATCCGCTACGAGATTTTGTGTTTCCCGGAAATATGCTTAACATTAAT 3360
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| | | | |
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| | | | |
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| | | | |
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Db 3661 ACAGGAAAGATGAGGAAAGCTAGGCCAACAAATTAAGGCTCTGCTGTGATTTACGATTT 3720
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QY 3781 ACTTTTCGCTGTTTCTGATTTGCTCAAAAACCTTGAACCTTAATTTTCTGCTGCTG 3840
| | | | |
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Db 3841 GCTTACCTCCGCTGCTTCTTCCACATTTGCAAGTACCCCTGATTCGATTAATTAAT 3900
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QY 3901 TTTACCTTTAATCTGCTTTTGTGCTGCTTCAAACTCCGCAAAATTTCTGTAAGC 3960
| | | | |
Db 3901 TTTACCTTTAATCTGCTTTTGTGCTGCTTCAAACTCCGCAAAATTTCTGTAAGC 3960
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Oy	6181	ATATTGTGNGNCTCAAAATATGTTGGCAATACGCATCCTCAGATTGTGTTCGTGA	6240
Db	6181	ATATTGTGNGNCTCAAAATATGTTGGCAATACGCATCCTCAGATTGTGTTCGTGA	6240
Oy	6241	TGCTTGAATAATTTTCCATTTCCATCAATCAATAAGCAAAATCTMAAATGTGGTCTCGCA	6300
Db	6241	TGCTTGAATAATTTTCCATTTCCATCAATCAATAAGCAAAATCTMAAATGTGGTCTCGCA	6300
Oy	6301	GCGACACATCATGACGTGATCGTGCGGCAAGACCACACTCAGAAAACCTACGTTCTTTAAA	6360
Db	6301	GCGACACATCATGACGTGATCGTGCGGCAAGACCACACTCAGAAAACCTACGTTCTTTAAA	6360
Oy	6361	CAAATACATTTTTTAAGTATTTAGTATTTAAATAATGTGGTATAGCAAGCTTAGCGCTCT	6420
Db	6361	CAAATACATTTTTTAAGTATTTAGTATTTAAATAATGTGGTATAGCAAGCTTAGCGCTCT	6420
Oy	6421	TTTCAGTCGACAACTTCTAATTTAATCGCGGCGTCTTCAAAAAGCTGTTCTTTGAAA	6480
Db	6421	TTTCAGTCGACAACTTCTAATTTAATCGCGGCGTCTTCAAAAAGCTGTTCTTTGAAA	6480
Oy	6481	TATTAAGCTTTATATATTTATATATTTAAAAATTTGATTACATGATATCAAAAGCGACTA	6540
Db	6481	TATTAAGCTTTATATATTTATATATTTAAAAATTTGATTACATGATATCAAAAGCGACTA	6540
Oy	6541	GTTTGATATTAATAATATCA 6560	
Db	6541	GTTTGATATTAATAATATCA 6560	
 RESULT 2 AA054630 ID AA054630 standard; cDNA to mRNA; 1315 BP. XX AC AA054630; XX DE 23-JUN-1994 (first entry) XX DT 23-JUN-1994 (first entry) XX DE ced-9 coding sequence.			
KW		Cell death; senescence; programmed cell death; ced-9; myocardial infarction; stroke; brain injury; neurodegenerative disease; muscular degenerative disease; ageing; hypoxia; ischemia; toxemia;	
KW		Infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2; oncogene; ss.	
OS		Caenorhabditis elegans.	
XX			
FH	Key	Location/Qualifiers	
FT	CDS	7..846	
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FT		/product= Ced-9.	
PN	MO9325683-A.		
XX			
PD	23-DEC-1993.		
XX			
PF	14-JUN-1993;	93WO-US05651.	
XX			
PR	12-JUN-1992;	92US-0898933.	
PR	10-AUG-1992;	92US-0927681.	
XX			
PA	(MASI) MASSACHUSETTS INST TECHNOLOGY.		
XX			
PI	Hengartner M, Horvitz HR;		
XX			
DR	WPI; 1994-007540/01.		
DR	P-PSDB; AAR47343.		
XX			
PT	Caenorhabditis elegans cell death-protective gene - used to develop agents for preventing cell death or for reducing population of cells		
PT			
XX			

PS	Claim 3; Page 58-59; 112pp; English.
XX	ccd-9 is essential for C. elegans development and apparently
CC	functions by protecting cells during development from programmed
CC	cell death. ccd-9 was shown to function by antagonising the
CC	activities of cell death genes ccd-3 and ccd-4. The protein product
CC	of the human oncogene bcl-2 was found to have a similar sequence
CC	to the ccd-9 protein. The ccd-9 gene can be used for developing
CC	agents for treating a condition characterised by increased cell death
CC	such as myocardial infarction, stroke, traumatic brain injury,
CC	neurodegenerative disease, muscular degenerative disease, ageing,
CC	hypoxia, ischaemia, toxemia, infection or hair loss. It can also
CC	be used for reducing a population of cells in the treatment of
CC	neoplastic growth cancerous tissue, infected cells or autoreactive
CC	immune cells.
XX	
XX	Sequence 1315 BP; 362 A; 290 C; 315 G; 347 T; 1 other;
XX	
XX	Query Match 9.6%; Score 631; DB 15; Length 1315;
XX	Best Local Similarity 99.7%; Pred. No. 9, 8e-123;
XX	Matches 631; Conservative 1; Mismatches 1; Indels 0; Gaps 0
QY	3393 GAGCAGCTTCATACACCTCGGAAACAAATGAAAGAGGACTACGAACGACGAGACCTGA 3452
DB	669 GAGCAGCTTCATACACCTCGGAAACAAATGAAAGAGGACTACGAACGACGAGACCTGA 728
QY	3453 AAAAGTGGGACGGCCGAGACAGAACAGAGCGTGTCGATGATTTGGCGCGGAGTACACG 3512
DB	729 AAAAGTGGGACGGCCGAGACAGAACAGAGCGTGTCGATGATTTGGCGCGGAGTACACG 788
QY	3513 TGGAGCATTGGAATGCTGTTGAGTGCCTGCTGTGTGGCGGATGATGCTTGAAGTA 3572
DB	789 TGGAGCATTGGAATGCTGTTGAGTGCCTGCTGTGTGGCGGATGATGCTTGAAGTA 848
QY	3573 ACGATTCATTAATTTGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3632
DB	849 ACGATTCATTAATTTGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
QY	3633 TTTGCTACGTATCTCTCATCCTTTGAACCTGGAGAAAGTGGAAAGCTAGGCCCAAT 3692
DB	909 TTTGCTACGTATCTCTCATCCTTTGAACCTGGAGAAAGTGGAAAGCTAGGCCCAAT 968
QY	3693 TACGGTCTCTGTGTGATTTACGATTTTACGCAATTTTTCGATTCGCTTTTCTTTT 3752
DB	969 TACGGTCTCTGTGTGATTTACGATTTTACGCAATTTTTCGATTCGCTTTTCTTTT 1028
QY	3753 GGCCAACCCCTACTCCGCGATATCAACTTTCCGTTGCTGTGACATTTGCTGTGACAAA 3812
DB	1029 GGCCAACCCCTACTCCGCGATATCAACTTTTCGTTGCTGTGACATTTGCTGTGACAAA 1088
QY	3813 CCCTGAACCTTAATTTTCTGCGCGTGAGCCCTCCGCTTCTCTTCCACATTTTCCA 3872
DB	1089 CCCTGAACCTTAATTTTCTGCGCGTGAGCCCTCCGCTTCTCTTCCACATTTTCCA 1148
QY	3873 AAGTACCCCTGATCTCAATATATCTTCACTTAATCTGTCTTTTCTGTGCGCTC 3932
DB	1149 AAGTACCCCTGATCTCAATATATCTTCACTTAATCTGTCTTTTCTGTGCGCTC 1208
QY	3933 TTCAACCTCCGCCCAATTTCTGTACGCGTACGCGACTTTTATTTATTTTTCAAATT 3992
DB	1209 TTCAACCTCCGCCCAATTTCTGTACGCGTACGCGACTTTTATTTATTTTTCAAATT 1268
QY	3993 GTTTTCTCTCAACAACAACAAAAACGGTTC 4025
DB	1269 GTTTTCTCTCAACAACAACAAAAACGGTTC 1301
XX	
XX	RESULT 3
XX	AAT38196/c
XX	AAT38196 standard; DNA; 7653 BP.
XX	AAT38196;
XX	

DT	17-DEC-1996	(first entry)
XX	Nematode Ced-3 gene.	
XX	Ced-3; interleukin-1 beta converting enzyme; ICE; protease	
KW	cell death; apoptosis; neural degeneration; inflammation;	
KW	antiinflammatory; ds.	
XX		
OS	Caenorhabditis elegans.	
XX		
FH	Key	Location/Qualifiers
FT	repeat_unit	1356..1472
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FT		/label= Repeat-1
FT	repeat_unit	1490..1614
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FT		/label= Repeat-2
FT	exon	2167..2366
FT		/*tag= c
FT		/codon_start= 2232..2234
FT	allele	2310
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FT		/label= T(n1040)
FT		/note= "causes L27F mutation"
FT	intron	2367..2429
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FT		/label= Intron-1
FT	exon	2430..2575
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FT	allele	2487
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FT		/label= A(n718)
FT		/note= "causes G65R mutation"
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FT		/label= Intron-2
FT	exon	2854..3107
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FT	repeat_unit	3329..3396
FT		/*tag= l
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FT	repeat_unit	3487..3759
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FT		/label= Repeat-2
FT	repeat_unit	3782..4070
FT		/*tag= n
FT		/label= Repeat-2
FT	exon	4303..4633
FT		/*tag= o
FT		/label= Intron-4
FT	repeat_unit	4688..4719
FT		/*tag= q
FT		/label= Repeat-3
FT	repeat_unit	5221..5330
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FT		/label= Repeat-3
FT	exon	5546..5760
FT		/*tag= s
FT	allele	5757
FT		/*tag= t
FT		/label= A(n2433)
FT		/note= "causes G360S mutation"
FT	intron	5761..5814
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FT		/label= Intron-5

FT	exon	5815..55942	/*tag= v
FT		5940	
FT	allele	/*tag= v	
FT		/label= T(n1165)	
FT		/note= "Creates premature stop codon at 403"	
FT	intron	5943..6297	/*tag= x
FT		/label= intron-6	
FT		6062..6138	/*tag= y
FT	repeat_unit	/label= Repeat-4	
FT		6298..6537	/*tag= z
FT	exon	6322	/*tag= aa
FT	allele	/label= T(n1949)	
FT		/note= "Creates premature stop codon at 412"	
FT		6372	
FT	allele	/*tag= ab	
FT		/label= A(n1286)	
FT		6434	/*tag= ac
FT	allele	/label= T(n1129,n1164)	
FT		/note= "causes A449V mutation"	
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FT	allele	/label= T(n2430)	
FT		/note= "causes A466V mutation"	
FT		6535	/*tag= ae
FT	allele	/label= A(n2426)	
FT		/note= "causes E483K mutation"	
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FT		6905..6965	/*tag= ah
FT	repeat_unit	/label= Repeat-5	
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FT		/note= "causes S486F mutation"	
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PN	WO9625946-A1.		
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PD	29-AUG-1996.		
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PE	23-FEB-1996;	96WO-US02473.	
XX			
PR	24-FEB-1995;	95US-0394189.	
XX			
PA	(MAST) MASSACHUSETTS INST TECHNOLOGY.		
XX			
PI	Horvitz HR, Shaham S, Yuan J;		
XX			
DR	WPI: 1996-425082/42.		
XX	P-PSDB; AAR98754.		
XX			
PT	Ced-3 and human interleukin 1-beta convertase genes and proteins		
PT	useful to treat inflammation and diseases characterised by cell		
PT	death		
XX			
PS	Claim 18; Fig 3; 139pp; English.		
XX			
CC	The Caenorhabditis elegans ced-3 gene (AAT38196) was cloned by		
CC	mapping RFLPs and chromosome walking, and genomic DNA cloned		

CC In plasmid pU107 was sequenced. EMS-induced alleles were also
 CC sequenced. The gene codes for a cell death protein (AA98754) that
 CC is structurally similar to human interleukin-1 beta converting
 CC enzyme (ICE) (AA98755), suggesting that Ced-3 protein may be a
 CC cysteine protease like ICE and that ICE may be a human equivalent
 CC of the nematode cell death gene. The ced-3 gene can be used as a
 CC probe or in the prodn. of Ced-3 protein and novel drugs for
 CC enhancing or inhibiting the activity of ICE, ced-3 and related
 CC genes for the treatment of inflammatory diseases and/or diseases
 CC caused by cell death. Novel inhibitors of ced-3 activity include
 CC portions of the ced-3 gene and its product.

SO Sequence 7653 BP; 2429 A; 1456 C; 1270 G; 2498 T; 0 other;

Query Match 2.1%; Score 139.2; DB 17; Length 7653;
 Best Local Similarity 73.3%; Pred NO.3.5e-19;
 Matches 211; Conservative 0; Mismatches 63; Indels 14; Gaps 2;

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 DB 1635 TGAATATTATACGGAACACAAATTCAGAGATGCGTATTACAGCATATTGGCGCC 1576
 QY 3123 AAAATATCCAGTAGAGAACTACAGTAATCTTTAAAT-----TTTAAATTTTAC 3176
 DB 1575 AAAATATCTGCTAGCTAGAACTACAGTAATCTTTAAATGACTAGCTGCGTGTGACG 1516
 QY 3177 AATTAAAGAAATACCACTAATCAAGAAATTAATTCAGAAATTCGAGCGGTAATC 3236
 DB 1515 ATTTCAGCGTTATCAAAATTCGAAAAAATTAATTTTCAAAATTCGAGCGTAATC 1456
 QY 3237 GA-----CTACAGTAGGCAATTTAAAGATTTAGATTTTGGTACGATATTTC 3288
 DB 1455 GACACAAAGCGCTACAGTACATCAATTAAGAAATTTAGGTTTGGTACGAGATTTT 1396
 QY 3289 CGCCTCAATATGTTGTGAATACGATTCAGGATTTTGGTCC 3336
 DB 1395 GCGGTCAATATGTTGCGCAGTACCATTTCTAGATTTTGATTC 1348

RESULT 4

AAAT72802/c
 ID AAAT72802 standard; DNA; 7653 BP.

AC AAAT72802;

DE 09-FEB-2001 (first entry)

DE ced-3 gene.

XX ced-3; virally induced cell death; apoptosis; gene therapy; neural;
 KW muscular degenerative disease; myocardial infarction; stroke; aging;
 KW interleukin-1beta converting enzyme; ICE; cysteine protease;
 KW Ice-ced 3 homologue; Ich; ds.

OS Caenorhabditis elegans.

XX Key Location/Qualifiers
 FH misc_signal 2161..2164

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 label= SL1_splice_acceptor_site

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 product= "Ced-3"

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FT exon /*tag= d
 number= 1

FT intron /*tag= e
 number= 2

FT intron /*tag= f
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 FT /*tag= h
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 FT 4635..5546
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 FT 5547..5760
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 FT 5815..5942
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PN US6083735-A.

PD 04-JUL-2000.

PE 10-JUN-1994; 94US-0258287.

PR 24-JUN-1993; 93US-0080850.

PA (GEHO) GEN HOSPITAL CORP.

XX Yuan J, Mura M;

XX WPI: 2000-464343/40.

DR P-PSDB; AAB14245.

PT New human Ich-1L and Ich-1S proteins for negative and positive
 PT regulation of programmed cell death and for developing therapeutic
 PT methods for diseases and conditions characterized by cell death, e.g.
 PT myocardial infarction or stroke

PS Example 1; Fig 2; 121pp; English.

XX The present sequence is the ced-3 gene from *Caenorhabditis elegans*.
 CC Structural analysis of this gene revealed that it is similar to the
 CC enzyme interleukin-1beta converting enzyme (ICE) gene and so it is
 CC thought that Ced-3 acts as a cysteine protease in controlling the onset
 CC of programmed cell death (apoptosis). The ced-3 gene may be used in gene
 CC therapy in disorders characterized by cell death e.g. neural and
 CC muscular degenerative diseases, myocardial infarction, stroke, virally
 CC induced cell death and aging. The present invention relates to a novel
 CC human Ice-ced 3 homologue (Ich) gene (AAAT72836), which is homologous to
 CC the ced-3 gene.

SO Sequence 7653 BP; 2429 A; 1455 C; 1271 G; 2498 T; 0 other;

Query Match 2.1%; Score 139.2; DB 21; Length 7653;


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FT      /tag= w
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FT      Intron 6538..7012
FT      /tag= x
FT      /number= Intron_7
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FT      repeat_unit 6905..6965
FT      /tag= z
FT      /rpl_type= INVERTED
FT      /note= "Inverted w.r.t. repeat 6567-6625"
FT      exon 7012..7075
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FT      /number= Exon_8
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FT      23-DEC-1993.
FT      14-JUN-1993: 93WO-0505701.
FT      12-JUN-1992: 92US-0897788.
FT      20-NOV-1992: 92US-0979638.
FT      (MASI ) MASSACHUSETTS INST TECHNOLOGY.
FT      Horvitz HR, Shaham S, Yuan J;
FT      WPI: 1994-007542/01.
FT      P-PSDB: AAR53281.
FT      Isolated C elegans cell death genes ced-3 and ced-4 - used to
FT      develop agents to increase or prevent cell death in organisms
FT      PS
FT      Claim 14; Fig 4; 127pp; English.
XX
XX      The sequences given in AA064735-45 represent mutations of the C. elegans
XX      ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
XX      was most abundant in embryos, but was also detected in larvae and young
XX      adults, suggesting that ced-3 is expressed not only in cells undergoing
XX      cell death. The four largest introns as well as sequences 5' of the
XX      start codon contain repetitive elements, some of which have been
XX      characterised in non-coding regions of other C. elegans genes, such
XX      as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
XX      length. Ced-3 is highly hydrophilic with no significant hydrophobic
XX      region that might be a transmembrane region. One region of Ced-3 is
XX      very rich in serine. It is thought that this region is involved in
XX      protein-protein interactions, similar to acid blobs in transcription
XX      factors. Of the mutations which occur within the ced-3 gene, eight of
XX      the mutations are missense mutations, two are nonsense mutations and
XX      two are putative splicing mutations. These mutations establish the
XX      null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
XX      function is not essential for viability. The ced-3 and ced-4 gene
XX      products may be used to develop agents for treating conditions
XX      characterised by cell deaths, such as myocardial infarction, stroke,
XX      degenerative disease, traumatic brain injury, hypoxia, pathogenic
XX      infection, aging or hair loss.
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XX      Sequence 7653 BP; 2430 A; 1453 C; 1271 G; 2499 T; 0 other;
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Query Match 2.1%; Score 137.6; DB 15; Length 7653;
Best Local Similarity 72.9%; Pred. No. 7.6e-19;
Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;
QY 3063 TGTATTGTTACGGAGATACAAATTCGAGATCTATTTCACACATATTGACGCGC 3122
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RESULT 7
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ID      AA064738 standard; DNA; 7653 BP.
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XX      AA064738;
AC
XX      23-JUN-1994 (first entry)
DT
XX      ced-3 (C5940T) gene.
DE
XX
XX      C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
XX      embryogenesis; cell death; hydrophilic; transmembrane; region;
XX      hydrophobic; mutation; amino acid; substitution; RNA splicing;
XX      protein synthesis; null phenotype; calcium-binding domain; ss.
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XX      Caenorhabditis elegans.
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FT      /tag= e
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FT      2576..2853
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PT develop agents to increase or prevent cell death in organisms
XX Claim 14; Fig 4; 127pp; English.
PS
XX
CC The sequences given in AA064735-45 represent mutations of the C. elegans
CC ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
CC was most abundant in embryos, but was also detected in larvae and young
CC adults, suggesting that ced-3 is expressed not only in cells undergoing
CC cell death. The four largest introns as well as sequences 5' of the
CC start codon contain repetitive elements, some of which have been
CC characterised in non-coding regions of other C. elegans genes, such
CC as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
CC length. Ced-3 is highly hydrophilic with no significant hydrophobic
CC region that might be a transmembrane region. One region of Ced-3 is
CC very rich in serine. It is thought that this region is involved in
CC protein-protein interactions, similar to acid blobs in transcription
CC factors. Of the mutations which occur within the ced-3 gene, eight of
CC the mutations are missense mutations, two are nonsense mutations and
CC two are putative splicing mutations. These mutations establish the
CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
CC function is not essential for viability. The ced-3 and ced-4 gene
CC products may be used to develop agents for treating conditions
CC characterised by cell deaths, such as myocardial infarction, stroke,
CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC infection, aging or hair loss.
XX
SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T; 0 other;
Query Match 2.1%; Score 137.6; DB 15; Length 7653;
Best Local Similarity 72.9%; Pred. No. 7.6e-19;
Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;
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DB 1635 TGAATTTATTACGAAACACAAATTCGAGAAATTCGATTAATTTGAGCGC 1576
QY 3123 AAAATATTCAGTAGGAAATCAATGATTTTAAAT-----TTTAAATTTTAC 3176
DB 1575 AAAATATTCGATGAGAACTACGATTAATTTTAAATGATGATGATGATGATGATG 1516
QY 3177 AATTAAGAAATTAACGATTAATCAAAAGAAATTAATTTCAAAATCGACCGTAAAC 3236
DB 1515 ATTTACGGGTTATCAAAATTCGAAATTTATTTTAAATTTGAGCGCGC 1456
QY 3237 GA-----CTACAGTAGGCAATTAAGATTTTCCCTAGGATTTTC 3288
DB 1455 GACACAAAGCGCTACAGTAGCATTTAAAGAAATTAATTTTCCCTAGGATTTTC 1396
QY 3289 GCGCTCAATATGTTGGAATATCGCATTCAGGATTTTGGTCC 3336
DB 1395 GCGCTCAATATGTTGCGCAGTAGCATTTTCAGAAATTTTGGATTC 1348

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RESULT 8

AA064739/c
ID AA064739 standard; DNA; 7653 BP.

AA064739;

23-JUN-1994 (first entry)

ced-3 (G6297A) gene.

C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
embryogenesis; cell death; hydrophilic; transmembrane; region;
hydrophobic; mutation; amino acid; substitution; RNA splicing;
protein synthesis; null phenotype; calcium-binding domain; ss.
Caenorhabditis elegans.

Key Location/Qualifiers
FT repeat_unit 1356..1472
FT //tag= a

Isolated C elegans cell death genes ced-3 and ced-4 - used to

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DB	1515	ATTTCAGGGTTACCAAAATTCGAAAAAAAATTAATTTTCAAAAATTGAGCCGTAAATC	1456
OY	3237	GA-----CTACAGTAGCATTTAAGAAATTAAGTAATCTAGTTCGCTACAGATTAATTC	3288
DB	1455	GACACAAGCGCTACAGTAGTATTAATTAAGAAATTTCTGTAGTTTCGCTACAGATTAATTT	1396
OY	3289	CGCCTCAAAATATGTTGTGAATATACGATTCACGAGATTTTGTGTCC	3336
DB	1395	GCCGTCAAAATATGTTGGCAGTACGATTCACAAATTTGTGATTC	1348
RESULT 9			
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XX			
DT	23-JUN-1994	(first entry)	
XX			
DE	ced-3 (C6322T) gene.		
XX			
KW	C. elegans; ced-4; ced-3; mutant; transcriptional regulation;		
KW	emryrogenesis; cell death; hydrophilic; transmembrane; region;		
KW	hydrophobic; mutation; amino acid; substitution; RNA splicing;		
KW	protein synthesis; null phenotype; calcium-binding domain; ss.		
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OS	Caenorhabditis elegans.		
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FH	Key	Location/Qualifiers	
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PR	20-NOV-1992;	92US-0979638.
XX		
PA	(MASI) MASSACHUSETTS INST TECHNOLOGY.	
XX		
PI	Horvitz HR, Shahan S, Yuan J;	
XX		
DR	WPI; 1994-007542/01.	
DR	P-PSDB; AAR53283.	
XX		
PT	Isolated C elegans cell death genes <i>ced-3</i> and <i>ced-4</i> - used to	
PT	develop agents to increase or prevent cell death in organisms	
XX		
PS	Claim 14; Fig 4; 127pp; English.	
XX		
CC	The sequences given in AA064735-45 represent mutations of the C. elegans	
CC	<i>ced-3</i> gene. A 2.8 kb mRNA was identified as the <i>ced-3</i> transcript and	

The sequences given in AA064735-45 represent mutations of the *C. elegans* *ced-3* gene. A 2.8 kb mRNA was identified as the *ced-3* transcript and

CC was most abundant in embryos, but was also detected in larvae and young
CC adults, suggesting that ced-3 is expressed not only in cells undergoing
CC cell death. The four largest introns as well as sequences 5' of the
CC start codon contain repetitive elements, some of which have been
CC characterised in non-coding regions of other *C. elegans* genes, such
CC as *ced-1*, *lin-12* and *myoD*. The *Ced-3* protein is 503 amino acids in
CC length. *Ced-3* is highly hydrophilic with no significant hydrophobic
CC region that might be a transmembrane region. One region of *Ced-3* is
CC very rich in serine. It is thought that this region is involved in
CC protein-protein interactions, similar to acid blobs in transcription
CC factors. Of the mutations which occur within the *ced-3* gene, eight of
CC the mutations are missense mutations, two are nonsense mutations and
CC two are putative splicing mutations. These mutations establish the
CC null phenotype of the *ced-3* gene, confirming that *ced-3*, like *ced-4*,
CC function is not essential for viability. The *ced-3* and *ced-4* gene
CC products may be used to develop agents for treating conditions
CC characterised by cell deaths, such as myocardial infarction, stroke,
CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC infection, aging or hair loss.

CC
XX
SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T; 0 other;

Query Match 2.1%; Score 137.6; DB 15; Length 7653;
Best Local Similarity 72.9%; Pred. No. 7.6e-19;
Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;

OY 3063 TGTATGTTACGGAATCAAAATTCGCAATGCTATTTCACAAATATTGACGGC 3122
DB 1635 TGAATATTATACGAAACAAATTCAGAAATGCGTATTACAGCATATTGCGCGC 1576
OY 3123 AAAATATCCAGTACGAGAAATCTACATATCTTTAAAT-----TTTAAATTTTAC 3176
DB 1575 AAATATGTCGTACGAGAAATCTACATATCTTTAAATGACTACTGTGCGTTGACG 1516
OY 3177 AATTAAAGAAATATACCACTAATCAAAAGAAATTAATTCAAAAATGAGCCGTAATTC 3236
DB 1515 ATTATGCGGTTATCAAAATTCGAAATAATTTTCAAAATTTGAGCCGTAATTC 1456
OY 3237 GA-----CTACATGAGCAATTTAAAGAAATTTAGTGTTCCTCGAGATATTTC 3288
DB 1455 GACACAGACGCTACAGTACATTTAAAGAAATTTAGTGTTCCTCGAGATATTTC 1396
OY 3289 CGCCTCAATATGTTGGAATATGCAATTCACGATTTTGTGTCC 3336
DB 1395 GCCGTCAATATGTTGCCGACATGCTTCAGAAATTTGTGATTC 1348

RESULT 10

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XX AC AA064741;

XX DT 23-JUN-1994 (first entry)

XX DE ced-3 (G6372A) gene.

XX C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
XX embryogenesis; cell death; hydrophilic; transmembrane; region;
XX hydrophobic; mutation; amino acid; substitution; RNA splicing;
XX protein synthesis; null phenotype; calcium-binding domain; ss.
XX
OS *Caenorhabditis elegans*.

XX Key Location/Qualifiers

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XX /note= "Inverted w.r.t. repeat at 1490-1614"

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XX      (MASI ) MASSACHUSETTS INST TECHNOLOGY.
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Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;

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Db      1455 GACACAGCGGTACAGTAGCTATTAAAGATTCAGTATTCGCTACAGATATTTT 1396
QY      3289 GCCTCAAAATATGTTGTAATATACCATTCACGAGATTTTGTGTCC 3336
Db      1395 GCCGTCAAAATATGTTGGCGAGTACGCATTCACAGATTTGTGATTTCC 1348

RESULT 11
AA064742/C
ID      AA064742 standard; DNA; 7653 BP.
XX
AC      AA064742;
XX
DT      23-JUN-1994 (first entry)
XX
DE      ced-3 (C6434T) gene.
XX
KW      C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
KW      embryogenesis; cell death; hydrophilic; transmembrane; region;
KW      hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW      protein synthesis; null phenotype; calcium-binding domain; ss.
XX
OS      Caenorhabditis elegans.
XX
FH      Key
FT      repeat_unit
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FT      /tag= a
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FT      /note= "Inverted w.r.t. repeat at 1490-1614"
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FT FT      repeat_unit      /number= Intron_4
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FT FT      /tag= s
FT FT      exon             5815..5942
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FT FT      /tag= t
FT FT      Intron           5943..6297
FT FT      /number= Intron_6
FT FT      /tag= u
FT FT      repeat_region    6062..6138
FT FT      /rpt_type= INVERTED
FT FT      exon             6298..6537
FT FT      /tag= v
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FT FT      mutation         6434
FT FT      /tag= w
FT FT      /note= "C>T, from allele n1129 and n1164"
FT FT      Intron           6538..7012
FT FT      /tag= x
FT FT      /number= Intron_7
FT FT      /tag= y
FT FT      repeat_unit      6567..6625
FT FT      /rpt_type= INVERTED
FT FT      /note= "Inverted w.r.t. repeat at 6905-6965"
FT FT      /tag= z
FT FT      /rpt_type= INVERTED
FT FT      /note= "Inverted w.r.t. repeat 6567-6625"
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FT FT      /tag= aa
FT FT      /number= Exon_8
FT FT      PN              WO9325685-A.
FT FT      XX              23-DEC-1993.
FT FT      PD              14-JUN-1993; 93MO-US05701.
FT FT      PE              12-JUN-1992; 92US-0897788.
FT FT      PR              20-NOV-1992; 92US-0979638.
FT FT      XX              (MASI ) MASSACHUSETTS INST TECHNOLOGY.
FT FT      PA              Horvitz HR, Shahan S, Yuan J;
FT FT      PI              WPI, 1994-007542/01.
FT FT      DR              P-PSDB; AAR53285.
FT FT      XX              Isolated C elegans cell death genes ced-3 and ced-4 - used to
FT FT      PT              develop agents to increase or prevent cell death in organisms
FT FT      XX              Claim 14; Fig 4; 127pp; English.
FT FT      PS              The sequences given in AA064735-45 represent mutations of the C. elegans
FT FT      CC              ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
FT FT      CC              was most abundant in embryos, but was also detected in larvae and young
FT FT      CC              adults, suggesting that ced-3 is expressed not only in cells undergoing
FT FT      CC              cell death. The four largest introns as well as sequences 5' of the
FT FT      CC              start codon contain repetitive elements, some of which have been
FT FT      CC              characterised in non-coding regions of other C. elegans genes, such

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CC as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
CC length. Ced-3 is highly hydrophilic with no significant hydrophobic
CC region that might be a transmembrane region. One region of Ced-3 is
CC very rich in serine. It is thought that this region is involved in
CC protein-protein interactions, similar to acid blobs in transcription
CC factors. Of the mutations which occur within the ced-3 gene, eight of
CC the mutations are missense mutations, two are nonsense mutations and
CC two are putative splicing mutations. These mutations establish the
CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
CC function is not essential for viability. The ced-3 and ced-4 gene
CC products may be used to develop agents for treating conditions
CC characterised by cell deaths, such as myocardial infarction, stroke,
CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC infection, aging or hair loss.
CC
XX
SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T; 0 other;
Query Match 2.18; Score 137.6; DB 15; Length 7653;
Best Local Similarity 72.94; Pred. No. 7,6e-19;
Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;
OY 3063 TGTATTGTTACGGGAATACAAATTCGACAAATGCTATTTCACAACTATTGACGCGC 3122
DB 1635 TGAATATTATTACGGAACACAAATTCAGAAATGCTATTACAGTATATTGGCCGC 1576
OY 3123 AAAATATCCAGTAGAAGAAACTACAGTAATCTTTAAAT-----TTTAAATTTTAC 3176
DB 1575 AAAATATGCTAGCTAGTAACATACAGTAATCTTTAAATGCTACTAGCTGTGACG 1516
OY 3177 AATTAAAGAAATTAACCACTAATCAAAAGAAATTAATTCAAAATGACGCCGTAATC 3236
DB 1515 AATTACGGGTTATCAAAATTCGAAAAAAATTTATTTTCAAAATTGAGCCGTAATC 1456
OY 3237 GA-----CTACAGTGGCATTTAAAGATTTCTGAGTTTCGACAGATATTTC 3288
DB 1455 GACACAGCGCTACAGTGTGTAATTAAGAAATCTGTAGTTTCGTCACAGATATTTC 1396
OY 3289 GCCCTCAATATGTTGTAATACGATTCACGGATTTTGTGTGCC 3336
DB 1395 GCCGTCAATATGTTGCCAGTCCGATTCAGAAATTTTGTGATTC 1348
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ID AA064743 standard; DNA: 7653 BP.
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AC AA064743;
XX
DT 23-JUN-1994 (first entry)
XX
DE ced-3 (C6485T) gene.
XX
KW C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
KW embryogenesis; cell death; hydrophilic; transmembrane; region;
KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW protein synthesis; null phenotype; calcium-binding domain; ss.
XX
OS Caenorhabditis elegans.
XX
XX
FH Key Location/Qualifiers
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FT /rpt_type= INVERTED
FT /note= "Inverted w.r.t. repeat at 1490-1614"
FT repeat_unit 1490..1614
FT /tag= b
FT /rpt_type= INVERTED
FT /note= "Inverted w.r.t. repeat at 1356-1472"
FT exon 2232..2366
FT /tag= c
FT /number= Exon_1
FT 2367..2429
FT /tag= d
FT Intron

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FT /number= Exon_2
FT 2576..2853
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FT /number= Intron_2
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FT /*tag= g
FT /number= Exon_3
FT 3108..4302
FT /*tag= h
FT /number= Intron_3
FT 3126..3243
FT /*tag= i
FT /rpl_type= INVERTED
FT /note= "Inverted w.r.t. repeat at 3329-3396"
FT 3329..3396
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FT /note= "Inverted w.r.t. repeat at 3126-3243"
FT 3487..3759
FT /*tag= k
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FT /note= "Inverted w.r.t. repeat at 3782-4070"
FT 3782..4070
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FT /rpl_type= INVERTED
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FT /*tag= m
FT /number= Exon_4
FT 4635..5546
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FT /rpl_type= INVERTED
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FT 5221..5330
FT /*tag= p
FT /rpl_type= INVERTED
FT /note= "Repeat 3"
FT 5547..5760
FT /*tag= q
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FT 5815..5942
FT /*tag= s
FT /number= Exon_6
FT 5943..6297
FT /*tag= t
FT /number= Intron_6
FT 6062..6138
FT /*tag= u
FT /rpl_type= INVERTED
FT 6298..6537
FT /*tag= v
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FT 6538..7012
FT /*tag= x
FT /number= Intron_7
FT 6567..6625
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FT /note= "Inverted w.r.t. repeat at 6905-6965"
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FT /*tag= z

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FT /rpl_type= INVERTED
FT /note= "Inverted w.r.t. repeat 6567-6625"
FT 7012..7075
FT /*tag= aa
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FT 23-DEC-1993.
FT 14-JUN-1993; 93WO-US05701.
FT 12-JUN-1992; 92US-0897788.
FT 20-NOV-1992; 92US-0979638.
FT (MASI ) MASSACHUSETTS INST TECHNOLOGY.
FT Horvitz HR, Shahan S, Yuan J;
FT WPI; 1994-007542/01.
FT P-PSDB; AAR53286.
FT Isolated C elegans cell death genes ced-3 and ced-4 - used to
FT develop agents to increase or prevent cell death in organisms
FT Claim 14; Fig 4; 127P; English.
FT
FT The sequences given in A0664735-45 represent mutations of the C. elegans
FT ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
FT was most abundant in embryos, but was also detected in larvae and young
FT adults, suggesting that ced-3 is expressed not only in cells undergoing
FT cell death. The four largest introns as well as sequences 5' of the
FT start codon contain repetitive elements, some of which have been
FT characterised in non-coding regions of other C. elegans genes, such
FT as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
FT length. Ced-3 is highly hydrophilic with no significant hydrophobic
FT region that might be a transmembrane region. One region of Ced-3 is
FT very rich in serine. It is thought that this region is involved in
FT protein-protein interactions, similar to acid blobs in transcription
FT factors. Of the mutations which occur within the ced-3 gene, eight of
FT two are putative splicing mutations, two are nonsense mutations and
FT null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
FT function is not essential for viability. The ced-3 and ced-4 gene
FT products may be used to develop agents for treating conditions
FT characterised by cell deaths, such as myocardial infarction, stroke,
FT CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
FT XX infection, aging or hair loss.
FT
FT SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T; 0 other;
FT
FT Query Match
FT Best Local Similarity 2.1%; Score 137.6; DB 15; Length 7653;
FT Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;
FT
FT QY 3063 TGTATTGTAGCGGAATCAAAATTCGAGAACTCTTTCACACATATTACGGC 3122
FT II III III III III III III III III III III III III III
FT DB 1635 TGAATATTATAGGAAACCAAAATTCAGAGATCGGATTACAGTATATTGGCCGC 1576
FT QY 3123 AAATATTCAGTAGAGAAATACAGTATCTTTAAAT-----TTTAAATTTTAC 3176
FT III III III III III III III III III III III III III III
FT DB 1575 AAAATATGTCGATAGACAGTAACTCTTAATGACTACTGAGCTTGTTACG 1516
FT QY 3177 AATTAAGAAATTAACCCATATCAAAAGAAATTAATTTCAAAATGAGCCGTAATC 3236
FT I III I III I III I III I III I III I III I III I III I
FT DB 1515 ATTTCGGGTATCAAAATTCGAAAAAATAATTTCAAAATTTGACCCGTAATC 1456
FT QY 3237 GA-----CTACGATGCGCATTTAAGAAATTAAGTACTAGTTTCGTACGAGATATTC 3288
FT I III I III I III I III I III I III I III I III I III I
FT DB 1455 GACACAGCGCTACAGTATCAATTTAAAGAAATTAAGTACTAGTTTCGTACGAGATATTTT 1396
FT QY 3289 GCGCTCAATATGTTGTAATAGCAATTCAGGATTTTGTGTTCC 3336
FT I III III III III I III III III I III III III I

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DB 1395 GCGGTCAATATGTCGCCAGTACGCAATTCGAGAAATTTTGATTC 1348

RESULT 13
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ID AA064744 standard; DNA; 7653 BP.

AC AA064744;
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XX 23-JUN-1994 (first entry)
XX
XX ccd-3 (G6536A) gene.
XX
XX C. elegans; ccd-4; ccd-3; mutant; transcriptional regulation;
XX
XX embryogenesis; cell death; hydrophilic; transmembrane; region;
XX
XX hydrophobic; mutation; amino acid; substitution; RNA splicing;
XX
XX protein synthesis; null phenotype; calcium-binding domain; ss.
XX
XX Caenorhabditis elegans.

OS
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FH 1356..1472
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FT /rpt_type= INVERTED
FT /note= "Inverted w.r.t repeat at 1490-1614"
FT 1490..1614
FT repeat_unit
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FT /rpt_type= INVERTED
FT /note= "Inverted w.r.t. repeat at 1356-1472"
FT 2232..2366
FT /tag= c
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FT /tag= e
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FT /number= Intron_2
FT 2854..3107
FT /tag= g
FT /number= Exon_3
FT 3108..4302
FT /tag= h
FT /number= Intron_3
FT 3126..3243
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FT /rpt_type= INVERTED
FT /note= "Inverted w.r.t. repeat at 3329-3396"
FT 3329..3396
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FT /rpt_type= INVERTED
FT /note= "Inverted w.r.t. repeat at 3126-3243"
FT 3487..3759
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FT /rpt_type= INVERTED
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FT 4303..4634
FT /tag= m
FT /number= Exon_4
FT 4635..5546
FT /tag= n
FT /number= Intron_4
FT 4688..4719
FT /tag= o
FT /rpt_type= INVERTED
FT /note= "Repeat 3"

FT repeat_unit 5221..5330
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FT /rpt_type= INVERTED
FT /note= "Repeat 3"
FT 5547..5760
FT /tag= q
FT /number= Exon_5
FT 5761..5814
FT /tag= r
FT /number= Intron_5
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FT /tag= s
FT /number= Exon_6
FT 5943..6297
FT /tag= t
FT /number= Intron_6
FT 6062..6138
FT /tag= u
FT /rpt_type= INVERTED
FT 6298..6537
FT /tag= v
FT /number= Exon_7
FT 6535
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FT /note= "G>A, from allele n2426"
FT 6538..7012
FT /tag= x
FT /number= Intron_7
FT 6567..6625
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FT /rpt_type= INVERTED
FT /note= "Inverted w.r.t. repeat at 6905-6965"
FT 6905..6965
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FT /note= "Inverted w.r.t. repeat 6567-6625"
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FT /tag= aa
FT /number= Exon_8
XX WO9325685-A.
XX 23-DEC-1993.
XX
XX 14-JUN-1993; 93WO-US05701.
XX
XX 12-JUN-1992; 92US-0897788.
XX 20-NOV-1992; 92US-0979638.
XX
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Horvitz HR, Shahan S, Yuan J;
XX
XX WPI; 1994-007542/01.
XX P-PSDB; AAR53287.
XX
XX Isolated C elegans cell death genes ccd-3 and ccd-4 - used to
XX develop agents to increase or prevent cell death in organisms
XX
XX Claim 14; Fig 4; 127pp; English.

The sequences given in AA064735-45 represent mutations of the C. elegans ccd-3 gene. A 2.8 kb mRNA was identified as the ccd-3 transcript and was most abundant in embryos, but was also detected in larvae and young adults, suggesting that ccd-3 is expressed not only in cells undergoing cell death. The four largest introns as well as sequences 5' of the start codon contain repetitive regions of other C. elegans genes, such as characterized in non-coding regions of other C. elegans genes, such as fem-1, lin-12 and myoD. The ccd-3 protein is 503 amino acids in length. Ccd-3 is highly hydrophilic with no significant hydrophobic region that might be a transmembrane region. One region of Ccd-3 is very rich in serine. It is thought that this region is involved in protein-protein interactions, similar to acid blobs in transcription

CC factors. Of the mutations which occur within the ced-3 gene, eight of
 CC the mutations are missense mutations, two are nonsense mutations and
 CC two are putative splicing mutations. These mutations establish the
 CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
 CC function is not essential for viability. The ced-3 and ced-4 gene
 CC products may be used to develop agents for treating conditions
 CC characterised by cell deaths, such as myocardial infarction, stroke,
 CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
 CC infection, aging or hair loss.

XX
 SQ Sequence 7653 BP: 2430 A; 1453 C; 1271 G; 2499 T; 0 other;

Query Match 2.1%; Score 137.6; DB 15; Length 7653;
 Best Local Similarity 72.9%; Pred. No. 7.6e-19;

Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;

OY 3063 TGTATTTTTCGGAATACAAATTCGAGATGCTATTTCACACATATTGACGCGC 3122
 DB 1635 TGAATTTTTCGGAATACAAATTCGAGATGCTATTTCACATATTGCGCGC 1576
 OY 3123 AAAATATCCAGTAGAAGAACTACAGTAATCTTTAAAT-----TTTAAATTTTAC 3176
 DB 1575 AAAAATATCTCGTAGCTACACTACGATATCTTTAAATGACTGAGCGCTTGACG 1516
 OY 3177 AATTAAAGAAATATACCACTAATCAAGAAATTAATTTCAAAATGAGCCGCTAATC 3236
 DB 1515 ATTTACGGGTATTCAGAAATTCGAAAAAATTAATTTTCAAAATTTGAGCCGCTAATC 1456
 OY 3237 GA-----CTACAGTAGGATTTAAAGATTTCTGATGTTTCGTACGATATTTC 3288
 DB 1455 GACACACGCTACAGTAGTATTAAAGAAATTTAGTGTGCTAGTTTCGTACGAGATTTT 1396
 OY 3289 CGCCTCAAAATATGTTGTAATACGATTCACGATTTTGTGTTCC 3336
 DB 1395 GCCGTCAAAATATGTTGGCAGTACGATTCACAAATTTTGTGTTCC 1348

RESULT 14
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 ID AAQ64745 standard; DNA: 7653 BP.

XX
 AC AAQ64745;

DT 23-JUN-1994 (first entry)

DE
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 XX ced-3 (C7020T) gene.

KW C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
 KW embryogenesis; cell death; hydrophilic; transmembrane; region;
 KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
 KW protein synthesis; null phenotype; calcium-binding domain; ss.
 XX
 OS Caenorhabditis elegans.

XX
 FH Key Location/Qualifiers
 FT repeat_unit 1356..1472

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 FT /rpl_type= INVERTED
 FT /note= "Inverted w.r.t. repeat at 1490-1614"
 FT repeat_unit 1490..1614

FT
 FT /tag= b
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 FT /note= "Inverted w.r.t. repeat at 1356-1472"
 FT exon 2232..2366

FT
 FT /tag= c
 FT /number= Exon_1
 FT intron 2367..2429

FT
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 FT exon 2450..2575
 FT /tag= e
 FT /number= Exon_2
 FT intron 2576..2853

FT /tag= f
 FT /number= Intron_2
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 FT /tag= g
 FT /number= Exon_3
 FT 3108..4302
 FT /tag= h
 FT /number= Intron_3
 FT 3126..3243
 FT /tag= i
 FT /rpl_type= INVERTED
 FT /note= "Inverted w.r.t. repeat at 3329-3396"
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 FT /rpl_type= INVERTED
 FT /note= "Inverted w.r.t. repeat at 3126-3243"
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 FT /note= "Inverted w.r.t. repeat at 3782-4070"
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 FT /note= "Inverted w.r.t. repeat 3487-3759"
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 FT /number= Exon_4
 FT 4635..5546
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 FT /number= Exon_7
 FT 6538..7012
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 FT 6567..6625
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 FT /rpl_type= INVERTED
 FT /note= "Inverted w.r.t. repeat at 6905-6965"
 FT repeat_unit 6905..6965
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XX PN WO325685-A.
 XX XX 23-DEC-1993.
 XX PF 14-JUN-1993; 93MO-US05701.
 XX PR 12-JUN-1992; 92US-0897788.
 XX PR 20-NOV-1992; 92US-0979638.
 XX PA (MAST) MASSACHUSETTS INST TECHNOLOGY.
 XX PI Horvitz HR, Shahan S, Yuan J;
 XX DR WPI, 1994-007542/01.
 XX DR P-PSDB; AAR53286.
 XX PS Isolated C elegans cell death genes ced-3 and ced-4 - used to
 PT develop agents to increase or prevent cell death in organisms
 XX
 PS Claim 14; Fig 4; 127pp; English.
 CC The sequences given in AA064735-45 represent mutations of the C. elegans
 CC ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
 CC was most abundant in embryos, but was also detected in larvae and young
 CC adults, suggesting that ced-3 is expressed not only in cells undergoing
 CC cell death. The four largest introns as well as sequences 5' of the
 CC start codon contain repetitive elements, some of which have been
 CC characterised in non-coding regions of other C. elegans genes, such
 CC as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
 CC length. Ced-3 is highly hydrophilic with no significant hydrophobic
 CC region that might be a transmembrane region. One region of ced-3 is
 CC very rich in serine. It is thought that this region is involved in
 CC protein-protein interactions, similar to acid blobs in transcription
 CC factors. Of the mutations which occur within the ced-3 gene, eight of
 CC the mutations are missense mutations, two are nonsense mutations and
 CC two are putative splicing mutations. These mutations establish the
 CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
 CC function is not essential for viability. The ced-3 and ced-4 gene
 CC products may be used to develop agents for treating conditions
 CC characterised by cell deaths, such as myocardial infarction, stroke,
 CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
 CC infection, aging or hair loss.
 XX
 SO Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T; 0 other;
 Query Match 2.1%; Score 137.6; DB 15; Length 7653;
 Best Local Similarity 72.9%; Pred. No. 7.6e-19;
 Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;

ID AA054401 standard; DNA; 7653 BP.
 XX AC AA054401;
 XX AC 01-JUL-1994 (first entry)
 XX DE ced-3 gene.
 XX KW C.elegans; cell death; gene; ced-3; inhibition; human; parasite;
 KW interleukin-beta convertase; ICE; pro-interleukin-beta; cytokine;
 KW inflammatory response; nematode; diagnosis; myocardial infarction;
 KW stroke; degenerative disease; traumatic brain injury; hypoxia; pest;
 KW pathogenic infection; hair loss; cancer; autoreactive antibody; ss.
 XX OS Caenorhabditis elegans.
 XX FH Key
 FT repeat_unit location/Qualifiers
 FT 1356..1472
 FT /tag= a
 FT /rpt_type= INVERTED
 FT /note= "Inverted w.r.t. repeat at 1490-1614"
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 FT /note= "Inverted w.r.t. repeat at 1356-1472"
 FT 2232..2366
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 FT /tag= d
 FT /note= "C>T, from allele n1040"
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 FT /tag= f
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 FT /note= "G>A, from allele n718"
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 FT 3487..3759
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FT intron
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PD 23-DEC-1993.
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PE 14-JUN-1993; 93WO-US05705.
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PR 12-JUN-1992; 92US-0897788.
PR 20-NOV-1992; 92US-0984182.
XX
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Horvitz HR, Shaham S, Yuan J;
XX
DR WPI: 1994-007551/01.
XX
DR P-PsDB; AAR45262.
XX
PT Agents which affect activity of cell death genes - used to
PT develop drugs for treating conditions characterised by cell death
PT or proliferation
XX
PS Disclosure; Fig 3; 132pp; English.
XX
CC This sequence encodes the C.elegans cell death gene, ced-3. Fragments
CC of the amino terminal of the protein encoded by this sequence act as
CC inhibitors of ced-3. This gene has considerable similarity to human
CC interleukin-1beta convertase (ICE), which converts pro-interleukin-
CC 1beta to the active cytokine and is involved in inflammatory response
CC in humans. The similarity between the two sequences suggests that
CC inhibitors of ced-3 may also act as inhibitors of ICE. Human ICE and
CC nematode Ced-3 proteins have an overall amino acid similarity of 28%.
CC The ced-3 inhibitors may be used for identifying agents which affect
CC the activity of a gene belonging to the to the ced-3/ICE family of
CC genes and for diagnosis of diseases characterised by cell death. They
CC can also be used to develop drugs for treating conditions characterised
CC by cell deaths such as myocardial infarction, stroke, degenerative
CC disease, traumatic brain injury, hypoxia, pathogenic infection, or
CC hair loss, or drugs for reducing the proliferative capacity or size
CC of a population of cells such as cancerous cells, cells which produce
CC autoreactive antibodies, infected cells, hair follicle cells or cells
CC which are critical to the life of a parasite, pest or recombinant
CC organism. They may also be used in the diagnosis of inflammatory
CC disease.
XX
SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T; 0 other;

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Query Match 2.1%; Score 137.6; DB 15; Length 7653;
Best Local Similarity 72.9%; Pred. No. 7.6e-19;
Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;

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QY 3063 TGTATTGTTAGCGGAATACAAATTCGCAATGCTATTTCACAACATATTGACGGGC 3122
DB 1635 TGAATATTATTCAGGAACCAAAATTCAGAAATGCGATTACAGTCATATTGCGCGCC 1576
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DB 1575 AAAATATCTCGTAGAGTAAGTAAGTAATCCTTAATAGACTAGTAGCGTTGTGACG 1516
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QY 3289 CGCCTCAATATATGTTGTGAATATGCAATTCACGGATTTTGTGTTCC 3336
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Search completed: February 27, 2003, 20:35:23
Job time : 1662.38 secs

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

February 27, 2003, 18:37:30 ; Search time 16061.4 seconds

(without alignments)
11886.551 Million cell updates/sec

Title: US-09-993-420A-1

Perfect score: 6560

Sequence: 1 atcgatagtcgtaccacaaat.....gtttgtataaaatratcaaa 6560

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_cm:*
- 5: gb_ov:*
- 6: gb_pal:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
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- 25: em_pl:*
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- 28: em_un:*
- 29: em_vl:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_lnv:*
- 33: em_htg_other:*
- 34: em_htg_mus:*
- 35: em_htg_pln:*
- 36: em_htg_rod:*
- 37: em_htg_mam:*
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- 41: em_htgo_mus:*
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- 43: em_htgo_rod:*
- 44: em_htgo_mam:*
- 45: em_htgo_vrt:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6539.8	99.7	7035	3	CELCTY1A
2	6395.8	97.5	33477	3	CELCTY1A
3	383.2	5.8	3419	3	CELCTY1A
4	174.8	2.7	894	3	CELCTY1A
5	171.2	2.6	152878	3	CELCTY1A
6	153.4	2.3	42430	3	CELCTY1A
7	149	2.3	34842	3	CELCTY1A
8	145	2.2	43525	3	CELCTY1A
9	145	2.2	257728	2	U88311
10	144.8	2.2	15033	3	CELCTY1A
11	143.6	2.2	122720	3	CELCTY1A
12	143.6	2.2	262336	2	AC006786
13	143.4	2.2	56448	3	AC006786
14	142.6	2.2	37794	3	U23139
15	142.6	2.2	309026	2	AC006786
16	142	2.2	36751	2	AC024770
17	140.4	2.1	110000	2	CELCTY1A
18	140.4	2.1	132742	3	CELCTY1A
19	139.4	2.1	33673	3	CELCTY1A
20	139.4	2.1	299015	2	AC006786
21	139.2	2.1	7653	3	CELCTY1A
22	139.2	2.1	7653	6	AR078185
23	139.2	2.1	7653	6	AR078185
24	139.2	2.1	13509	6	AR103124
25	139.2	2.1	13509	6	AR103124
26	139.2	2.1	33477	3	CELCTY1A
27	138.6	2.1	26354	3	CELCTY1A
28	137.2	2.1	36751	3	AC024770
29	137	2.1	152878	3	CELCTY1A
30	136.8	2.1	37310	3	CELCTY1A
31	136.8	2.1	38608	3	CELCTY1A
32	136	2.1	29122	3	CELCTY1A
33	135.2	2.1	26858	3	AC024811
34	135.2	2.1	260699	2	AC006874
35	135.2	2.1	306131	2	AC006874
36	135	2.1	23135	3	AC024770
37	135	2.1	122720	3	AC024770
38	135	2.1	132558	3	AC025721
39	134.6	2.1	42430	3	AF003386
40	133.4	2.0	40145	3	CEC36A4
41	133.2	2.0	39337	3	U39848
42	133.2	2.0	331326	2	AC006802
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44	132.8	2.0	33000	3	CEK11H3
45	131.8	2.0	58069	3	AC024775

ALIGNMENTS

RESULT 1
LOCUS CELCTY1A
DEFINITION Caenorhabditis elegans Cyt-1 (Cyt-1) and CED-9 (ced-9) genes,
complete cds; and unknown gene.
ACCESSION L26545
VERSION L26545.1
KEYWORDS GI:433174

SOURCE
ORGANISM Caenorhabditis elegans.

Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Rhabditidae; Rhabditidae; Pelodermidae; Caenorhabditis.

REFERENCE
1 (bases 1 to 7035)

Hengartner, M.O. and Horvitz, H.R.

C. elegans cell survival gene ced-9 encodes a functional homolog of

the mammalian proto-oncogene bcl-2
JOURNAL Cell 76 (4), 665-676 (1994)
MEDLINE 94170367
PUBMED 7907274
FEATURES

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Best local Similarity 100.0%; Pred. No. 0;
Matches 6558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATCGATAGTCTGCACCAATGATTTCCGATTCACAGTACGATGCTGCAATTTA 60
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Qy	121	TAATTTAAAAAATCAATTTGCATTTGAAATTCACACTCTCTAGTGTTTGAAAATGCAA	180
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Qy	241	TTGTAGTGAATTTCTCCCGCAAGAAATAGAACTTTGCAGATTCCTCGAGCGGAACGGAT	300
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Qy	301	TTTTSATPACAAAAAACTATTCAGAACCAATAGAGACTTTTTCMAATATTCCTATTATG	360
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Qy	421	AGGATAAAAGGCTCATTTTGAAGCCGAAATTTACTAAATCTCTAGCCTGAGTGCAT	480
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Qy	481	GGATCGGAATTCGAGGAATTTTAGATTTCACTCTGAATTTCCAAATGCAAAAAATAT	540
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Qy	541	ATTCAAGAAAAATCACAGAAATGCAACAAAAAACAACAAAAAAGAACAAAAACAAGC	600
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Qy	661	ACTTTCGTGCCCTGTGCGTGCATTTCCGCAACAAAATCAACACTGTGTTGANAACGA	720
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Qy	1021	CAGGCTCCAAAGATGGCCCAATTCGTCACATCTCCACGCTTACACGCCCAATTAAC	1080
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Db	1798	AATGTTGGACAGGTAGAGATTGAAATTTAAATTAATTTAATTTGTTTAAAAATTAATTAAT	1857
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Db	2398	ATTTTTTAATTTTTTTTTTGTAAATTAATAATTTCTGCTGCTTCACAGTGCATATTTCACG	2457
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Db	2458	CACGGAATCCGGCAAAAACGGAATGGAATGTTTGGAGACACCGGGATTTCCGTGTGGAGTG	2517
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RESULT 2
CE707C4
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DEFINITION
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ACCESSION
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VERSION
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KEYWORDS
HTG.
SOURCE
Caenorhabditis elegans.
ORGANISM
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Pelodermidae; Caenorhabditis.

REFERENCE
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TITLE
Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
Science 282 (5396), 2012-2018 (1998)
JOURNAL
MEDLINE
99069613
PUBMED
9851916
REMARK
The C. elegans Sequencing Consortium.
2 (bases 1 to 33477)
Berk, M.
Direct Submission
Submitted (18-JAN-1994) Nematode Sequencing Project, Sanger
Institute, Hinxton, Cambridge CB10 1SA, England and Department of
Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
On Nov 21, 1995 this sequence version replaced gi:443827.
Coding sequences below are predicted from computer analysis, using
predictions from GeneFinder (P. Green, U. Washington), and other
available information.
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is not the entire insert of clone T07C4.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.
The true left end of clone T07C4 is at 1 in this sequence. The true
left end of clone C38H2 is at 33374 in this sequence. The start of
this sequence (1..101) overlaps with the end of sequence Z48055.
The end of this sequence (33374..33477) overlaps with the start of
sequence Z35641.
For a graphical representation of this sequence and its analysis
see: [http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?](http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=T07C4)
name=T07C4
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
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CDS		join(13739..13883,14869..15116) /gene="T07C4.5" join(13739..13883,14869..15116) /gene="T07C4.5" /note="contains similarity to Pfam domain: PF01060 (Transhyretin-like family), Score=143.6, E-value=1.1e-39, N=1 cDNA EST EMBL:M79967 comes from this gene cDNA EST EMBL:M79968 comes from this gene cDNA EST YK445d4.3 comes from this gene cDNA EST YK445d4.5 comes from this gene cDNA EST YK542f9.3 comes from this gene cDNA EST YK542f9.5 comes from this gene /codon_start=1 /protein_id="CAAB2574.1" /db_xref="GI:3879512" /db_xref="SPTREMBL:O222288"		
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Oy	61	CAAAATCCGAGAAAAGAAGATGCAGAAGATGAAGAAGTCCGAAATCTAAATATT	120	
Db	9432	CAAAATCCGAGAAAAGAAGATGCAGAAGATGAAGAAGTCCGAAATCTAAATATT	9491	
Oy	121	TAAATTTAAAAAATCAATTTGCAATTGAATTCAACCCGACGCTTTGAAAAATGCCAA	180	
Db	9492	TAAATTTAAAAAATCAATTTGCAATTGAATTCAACCCGACGCTTTGAAAAATGCCAA	9551	

QY	181	TCCTTAAGTAACCTCTGATCGCCCAATTTCTTCACAAATTCCTTCAAGTAGTGTT	240
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QY	241	TTGTAAGTATTTCCCTCCGCAAAAGATAGGAACCTTTCGAACTCTCTGGAGGAACGGGAT	300
Db	9612	TTGTAAGTATTTCCCTCCGCAAAAGATAGGAACCTTTCGAACTCTCTGGAGGAACGGGAT	9671
QY	301	TTTATATACAAAAAACTATTCAGACAAACCATAGGACCTTTTCAAAATATCTCTATTATGG	360
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QY	480	TGGATCAGAAATTCGAGGAATTTTAGATTTCATCTTGAAATTTGCAATGAAAAAATAT	539
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Db	9972	CGAAAGTGCGCCCGGGTGCTTCTAGCCATCTCTTCAACAGAGAGCGCTCTGGCG	10031
QY	660	CACCTTCGTGCGCCGTGCGGCAATTTCCGCAACAAATTCGAACCTGTTTTAAACGC	719
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QY	720	ACCGCCGTGTTCTTTTTCATTTTGAATGATAGAAAAATCAGATTGTTCAAGATGATTAA	779
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QY	900	TTTGTTAGCGATGGAAGGAATGTATACACACATTTCTTTTCATTTAATTATTATTA	959
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QY	960	ATATTACAGTTCGAGGCAAAAGCGCAATCCAGAAGTTTCGATGGGAATACCTGTTGAA	1019
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Db	10512	CGGAGGATTCGGAATTCGCGAGTTTCCGCTTGATTTACCGCTTTTGTGGAATTCATCG	10571
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Oy 5875 GACAAATTTGGCAAGATATCTTTTGATATACAAATTAACGAAGTCAAGCAGAAAT 5934
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Oy 5995 GCG - AAACATACGATATTTCTCAAAAGACTACTAGCGCTTGCTGATTTAGAGCTC 6052
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Oy 6053 GATTTTGAATGAATCAGACTAGAGAAAGAGAGAAATATTTGACATCATTTGAACA 6112
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Oy 6113 TCAATTCAAAAGTGAACCCCTTGACTACAGTATCTTCTAAGAAATGATGTTTC 6172
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Db 15608 TCTCGTATGCTTGAATAATTTTCCATTTCAACATCAATAAAGCAATTTAAATGTGG 15667
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Oy 6473 TTTGAAATTTAAGCTTTATATATTTATATTTAATAATTTTGAATACGATATCAAA 6532
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Oy 6533 AGCGAGTAGTTGTATATAAAATTTATCA 6560
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ORGANISM *Caenorhabditis briggsae*
 Eukaryota; Metazoa; Chordata; Rhabditiida;
 Rhabditiida; Rhabditiidae; Peloderae; *Caenorhabditis*.
 1 (bases 1 to 3419)
 AUTHOR S. Hengartner, M.O. and Horvitz, H.R.
 C. elegans cell survival gene ced-9 encodes a functional homolog of
 the mammalian proto-oncogene bcl-2
 Cell 76 (4), 665-676 (1994)
 JOURNAL 94170367
 MEDLINE 94170367
 PUBMED 7907274

FEATURES

source	Location/Qualifiers
gene	1..3419 /organism="Caenorhabditis briggsae" /db_xref="taxon:6238"
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intron	1872..1873
exon	1873..2133
intron	2133..2187

RESULT 3

CELCHBO 3419 bp DNA linear INV 26-JUL-1994
 LOCUS *Caenorhabditis briggsae* (cyt-1) and (ced-9) genes, complete cds.
 DEFINITION complete cds.
 ACCESSION L26546.1 GI:450579
 VERSION L26546.1 GI:450579
 KEYWORDS *Caenorhabditis briggsae* DNA.

Query Match	5.88;	Score 383.2;	DB 3;	Length 3419;
Best Local Similarity	61.9%;	Pred. No. 2.5e-61;		
Matches 860; Conservative	0;	Mismatches 383;	Indels 147;	Gaps 10;

QY 963 TTCACATCCGAGGCAAGAGCGCAATCCGAGAGTTCCGATGGAAATACCTGTTGAAGCA 1022
 Db 775 TTTTCACTCGGAGGCAAGAGCTCTTATCCAAAGTTGGATGGGAATACCTCAAGAGCA 834
 QY 1023 GCCGTCCAGAAATCGCCCAATCGCTCCACATCTCACCTGCTTACACGCAACAATTGACCG 1082
 Db 835 GCGGAGCATGAAAGCGCCCGATCGCTCCACATCTCACCATCTACACGCAACAATCACTG 894
 QY 1083 GATGCTCTCGGAAATTCATATGATATCAGCGGTTGTGTAATGCGGGAACCTTCTGCTGG 1142
 Db 895 GATGCTTCTTGAAATTCACAGATCAGTATGATGCGGATGGCGGAAACCTTCTGTTGG 954
 QY 1143 AGGAATCGGAATTCGAGTTTGGCGTTTCATTTACACCGCTTTTGGAGATTATCCGAG 1202
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 Db 1484 TCGATTTATACCTGCTCTCTTTTCTTCTGTGAAATTAATCGTTTCTTTCCAAATGATAT 1543
 QY 1641 TTAATGAACGATTAATAATTTTA---GATGACAGCTCTCAAGCGGAGCAACTGCT-- 1694
 Db 1544 ATTTTAAACAAATTAATAATTTTATGATCATGACACGCGATGCAATGATGCTGATTCATGG 1603

QY	1695	-----GACGAATCCGGCCGTAATGGCGACGACACGATGGCGACTGGCGAGATGA	1741
Db	1604	ATATGCGAAACTGCTGGAGATACGTTCCGAGGGAGGACATATGGCCACACATGGTAATTA	1663
QY	1742	AGGACTTTCCTGGGGATATAAAGGCGACACAGCCCGACCGAATTTTGGAAATCATATGATGCTC	1801
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QY	1922	TTTTTATATTTTATTTTGTAAATAAATTTCTGGCTGCTCCAGGTGACATTTTTCACGC	1961
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QY	1962	ACCGAATCCGGCAAAACGCAATGGAATGGTTTGGACACCGGATTTGCCGTGGAGTGC	2041
Db	1889	ATCCGATAGCACAAAATGCTCTGATTTGATGATGCGCGTGCANTTACCAGATGGAATTC	1948
QY	2042	AACCGGACGCAAAATGATATGATCCGATTATGAGGAACATATTTGAGAGAACGCGGGAAA	2101
Db	1949	AAAAAGAGCATGATGATGATGCGATCATTTGGGAAACATTTTGGAAAAAGACATGAGGA	2008
QY	2102	ATTTTGAAGCTTCTGTGAGCAGCTGCTGCGACGTGCCGAGATCTCATTTTGCATCTATC	2161
Db	2009	TGTTGAAAACTTCTGTGAACAACACTTTCGCAATTCGCAAAAATTAAGTTTTCATTTGACC	2068
QY	2162	AGGATGTGCTTGGAGCGTGTGGAATGCAACAGACAGATCATGTCCATGTCTTATGAC	2221
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QY	2222	GTTTGGTAAG 2231	
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RESULT 4
D78157
LOCUS      D78157
DEFINITION Ascaris suum mitochondrial mRNA for cytochrome b-large subunit, complete cds.
ACCESSION D78157
VERSION   D78157
KEYWORDS  cytochrome b-large subunit.
SOURCE    Ascaris suum mitochondrion cDNA to mRNA.
ORGANISM  Mitochondrion Ascaris suum
           Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;
           Ascariidoidea; Ascariidae; Ascaris.
REFERENCE 1 (sites)
AUTHORS   Kita,K., Hirawake,H. and Takamiya,S.
TITLE     Cytochromes In the respiratory chain of helminth mitochondria International Journal for Parasitology (1997) In press
REFERENCE 2 (bases 1 to 894)
AUTHORS   Kita,K.
TITLE     cDNA cloning of cytochrome b large subunit of mitochondrial fumarate reductase from Ascaris suum
JOURNAL   Unpublished
REFERENCE 3 (bases 1 to 894)
AUTHORS   Kita,K.
TITLE     Direct Submission
JOURNAL   Submitted (25-OCT-1995) Kiyoshi Kita, The Institute of Medical Science, The University of Tokyo, Parasitology, 4-6-1 Shirokanedai, Minato-Ku, Tokyo 108, Japan (E-mail:kita@ims.u-tokyo.ac.jp, Tel:03-5449-5370, Fax:03-5449-5410)
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VERSION AF003386.1 GI:2088833
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 da; Rhabditiida; Rhabditiidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 42430)
 AUTHORS Waterston, R.
 TITLE Genome sequence of the nematode C. elegans: a platform for
 JOURNAL investigating biology. The C. elegans Sequencing Consortium
 MEDLINE Science 282 (5396), 2012-2018 (1998)
 PUBMED 9851916
 REFERENCE 2 (bases 1 to 42430)
 AUTHORS Johnson, D.
 TITLE The sequence of C. elegans cosmid F59E12
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 42430)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAY-1997)
 REFERENCE 4 (bases 1 to 42430)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2001) Department of Genetics, Washington
 University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
 Louis, MO 63110, USA
 REFERENCE 5 (bases 1 to 42430)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (21-SEP-2001) Department of Genetics, Washington
 University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
 Louis, MO 63110, USA
 REFERENCE 6 (bases 1 to 42430)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (05-OCT-2001) Department of Genetics, Washington
 University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
 Louis, MO 63110, USA
 REFERENCE 7 (bases 1 to 42430)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (22-MAY-2002) Department of Genetics, Washington
 University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
 Louis, MO 63110, USA
 COMMENT Submitted by:
 Genome Sequencing Center
 Department of Genetics, Washington University
 St. Louis, MO 63110, USA, and
 Sanger Centre, Hinxton Hall
 Cambridge CB10 1RQ, England
 email: twenematode.wustl.edu and jessesanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.
 It may be shorter because we only sequence overlapping sections
 once, or longer because we provide a small overlap between
 neighboring submissions.

This sequence was finished as follows unless otherwise noted: all
 regions were double stranded, sequenced with an alternate chemistry
 or covered by high quality data (i.e., phred quality >= 30); an
 attempt was made to resolve all sequencing problems, such as
 compressions and repeats; all regions were covered by sequence from
 more than one m3 subclone.

For a graphical representation of this cosmid sequence and its
 analysis see:
<http://www.wormbase.org/db/seq/sequence?name=F59E12;class=Sequence>

NEIGHBORING COSMID INFORMATION

The 5' cosmid is C17G10, 5100 bp overlap; the 3' cosmid is C25H3,
 200 bp overlap. Actual start of this cosmid is at base position

FEATURES

source
 misc_feature
 gene
 CDS
 2488 of F59E12; actual end is at 3056 of C25H3.
 NOTES:
 Coding sequences below are the result of integration and manual
 review of the following data: computer analysis using the program
 GeneFinder (P. Green and L. Hillier, personal communication), the
 large scale EST projects of Yujl Kohara
 (http://www.ddb.jnc.ac.jp/c-elegans/html/CE_INDEX.html) and The C.
 elegans ORPOME cloning project (<http://worldb.dic.harvard.edu/>),
 similarity to other proteins from Blastx analyses
 (<http://blast.wustl.edu/>), sequence conservation with C. briggsae
 using Jim Kent's WABA alignment program (Genome Research
 10:1115-1125, 2000), individual C. elegans GenBank submissions,
 and personal communications with C. elegans researchers. tRNAs
 are predicted using the program tRNAscan-SE (Lowe, T.M. and
 Eddy, S.R., 1997, Nucleic Acids. Res., 25, 955-964).
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Best Local Similarity 61.1%; Pred. No. 1.4e-18;
Matches 276; Conservative 0; Mismatches 173; Indels 3; Gaps 2;

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Db 17755 ATTTTCTCTGAAATTAATGCTGATGAAGACGATTAACCGACGCAAAATTTGAGATA 17814
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QY 4755 ATGAGCCCTTTAAAGAGCTGCTACTTTGAACCTTCTGTTCCGCACTTTTCATCGA 4814
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Db 17875 GTGTGCGCTTTTAAAGAGCTGATTTTCAATTTTAATTCGACGAATTTTCATCGA 17934
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Db 17935 TTTTTCATAGTTATTTGATGAACATATTTTATATATATATATATATATATATATATAT 17994
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FEATURES
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RESULT 7
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REMARK
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
    Direct Submission
    Submitted (30-JUN-1995) Nematode Sequencing Project, Sanger
    Institute, Hinxton, Cambridge CB10 1SA, England and Department of
    Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
    jess@anger.ac.uk or rwenematode.wustl.edu
    Coding sequences below are predicted from computer analysis, using
    predictions from GeneFinder (P. Green, U. Washington), and other
    available information.
    Current sequence finishing criteria for the C. elegans genome
    sequencing consortium are that all bases are either sequenced
    unambiguously on both strands, or on a single strand with both a
    dye primer and dye terminator reaction, from distinct subclones.
    Exceptions are indicated by an explicit note.
    This sequence is the entire insert of clone F54C9. The true right
    end of clone W01C9 is at 11134 in this sequence. The start of this
    sequence (1..101) overlaps with the end of sequence 24996.
    The end of this sequence (34733..34842) overlaps with the start of
    sequence 268315.
    For a graphical representation of this sequence and its analysis
    see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
    name=F54C9
    IMPORTANT: This sequence is NOT necessarily the entire insert of
    the specified clone. It may be shorter because we only sequence
    overlapping sections once, or longer because we arrange for a small
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JOURNAL REFERENCE AUTHORS TITLE JOURNAL	Unpublished 2 (bases 1 to 257728 Waterston, R.H. Direct Submission Submitted (24-FEB-1999
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COMMENT
MO 03108, USA
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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ORIGIN									

Query Match 2.2%; Score 145; DB 2; Length 257728
Best Local Similarity 62.3%; Pred. No. 4.4e-17;
Matches 308; Consensus 0

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QY	5057	ACATATTATGCGCA	5070		
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REFERENCE AUTHORS TITLE	REFERENCE AUTHORS TITLE
JOURNAL MEDLINE PUBMED	246793 246793.1 GI:577756 HTG, Lys-tRNA; Myosin regulatory light chain 2; transfer RNA Caenorhabditis elegans. Caenorhabditis elegans. Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea; Rhabditidae; Pelodolerinae; Caenorhabditis. 1 none.
REMARK REFERENCE AUTHORS TITLE JOURNAL	Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology. The <i>C. elegans</i> Sequencing Consortium Science 282 (5396), 2012-2018 (1998) 99069613 9851916 The <i>C. elegans</i> Sequencing Consortium. 2 (bases 1 to 15023) Percy C.M. Direct Submission Submitted (25-NOV-1994) Nematode Sequencing Project, Sanger

COMMENT

FEATURES

source

gene

CDS

RESULT 10	CEC5667/c	LOCUS	CEC5667	15023 bp	DNA	linear	INV 14-MAY-2002
DEFINITION	Caenorhabditis elegans cosmid C5667, complete sequence.						

DEFINITION Caenorhabditis elegans cosmid Y48G8AL, complete sequence.
 AC025721
 VERSION AC025721.2 GI:13559692
 KEYWORDS HTG.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Rhabditioidea; Rhabditidae; Pelodierinae; Caenorhabditis.
 REFERENCE
 AUTHORS 1 (bases 1 to 122720)
 TITLE Waterston, R.
 JOURNAL Genome sequence of the nematode C. elegans: a platform for
 MEDLINE investigating biology. The C. elegans Sequencing Consortium
 PUBMED 99069613
 9851916
 REFERENCE
 AUTHORS 2 (bases 1 to 122720)
 TITLE Murray, J. and Du, H.
 JOURNAL The sequence of C. elegans cosmid Y48G8AL
 UNPUBLISHED (2001)
 3 (bases 1 to 122720)
 REFERENCE
 AUTHORS Waterston, R. H.
 TITLE Direct Submission
 JOURNAL Submitted (12-MAR-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE
 AUTHORS 4 (bases 1 to 122720)
 TITLE Waterston, R.
 JOURNAL Direct Submission
 UNPUBLISHED (06-APR-2001) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 REFERENCE
 AUTHORS 5 (bases 1 to 122720)
 TITLE Waterston, R.
 JOURNAL Direct Submission
 UNPUBLISHED (07-SEP-2001) Department of Genetics, Washington
 University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
 Louis, MO 63110, USA
 REFERENCE
 AUTHORS 6 (bases 1 to 122720)
 TITLE Waterston, R.
 JOURNAL Direct Submission
 UNPUBLISHED (16-NOV-2001) Department of Genetics, Washington
 University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
 Louis, MO 63110, USA
 REFERENCE
 AUTHORS 7 (bases 1 to 122720)
 TITLE Waterston, R.
 JOURNAL Direct Submission
 UNPUBLISHED (19-APR-2002) Department of Genetics, Washington
 University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
 Louis, MO 63110, USA
 COMMENT On Apr 6, 2001 this sequence version replaced gi:7230345.
 Submitted by:
 Genome Sequencing Center
 Department of Genetics, Washington University
 St. Louis, MO 63110, USA, and
 Sanger Centre, Hinxton Hall
 Cambridge CB10 1RO, England
 email: twenematode.wustl.edu and jesusanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.
 It may be shorter because we only sequence overlapping sections
 once, or longer because we provide a small overlap between
 neighboring submissions.

This sequence was finished as follows unless otherwise noted: all
 regions were double stranded, sequenced with an alternate chemistry
 or covered by high quality data (i.e., phred quality >= 30); an
 attempt was made to resolve all sequencing problems, such as
 compressions and repeats; all regions were covered by sequence from
 more than one m13 subclone.

For a graphical representation of this cosmid sequence and its
 analysis see:
www.wormbase.org/db/seq/sequence?name=Y48G8AL;class=Sequence

NEIGHBORING COSMID INFORMATION

The 5' cosmid is 2K993, 200 bp overlap; the 3' cosmid is Y48G8AR,
 200 bp overlap.

NOTES:

Coding sequences below are the result of integration and manual
 review of the following data: computer analysis using the program
 GeneIndex (P. Green and L. Hillier, personal communication), the
 large scale EST projects of Yujl Kohara
 (http://www.dbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C.
 elegans ORFome cloning project (<http://worldb.dfci.harvard.edu/>),
 similarity to other proteins from Blastx analyses
 (<http://blast.wustl.edu/>), sequence conservation with C. briggsae
 using Jim Kent's WABA alignment program (Genome Research
 10:115-1125, 2000), individual C. elegans genbank submissions,
 and personal communications with C. elegans researchers. tRNAs
 are predicted using the program tRNAscan-SE (Lowe, T.M. and
 Eddy, S.R., 1997, Nucleic Acids. Res., 25, 955-964).

FEATURES

source

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/clone="Y48G8AL"

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Db	44798	TACGGAATCTCGATTTTGGGAGAGAA-----AATGAAATTCGAGCCCGTAATTCGACC	44744	
OY	3240	TACAGTAGCATTTAAAGAAATTCCTGTAATTTCCGTCAGAGATP-TTCCGCCTCAAT	3298	
Db	44743	TACAGTAGCATTTAAAGAAATTCGTAAGTTTCCGTCAGAGATATTTGGCGCTCAAT	44684	

Accession	Version	Keywords	Source	Organism	Reference	Journal	Reference	Authors	Title	Journal																																													
3299	ATGTTGTAATACGACATTCACGATTTTGTGTTCC	3336																																																					
44683	ATGTTGTGCATTAACGACATTTCTCAGAAATTTGTGTTCC	44646																																																					
RESULT 12	AC006786/c	LOCUS	DEFINITION	AC006786	262336 bp	DNA	linear	HTG 25-FEB-1999																																															
	Caenorhabditis elegans clone y48g8, ***	SEQUENCING	IN PROGRESS	13 unordered pieces.																																																			
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	Unpublished	2 (bases 1 to 262336)	Waterston, R.H.	Unpublished	2 (bases 1 to 262336)	Waterston, R.H.	Unpublished	2 (bases 1 to 262336)	Waterston, R.H.	Unpublished																																													
	Submitted (23-FEB-1999)	Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	On Mar 1, 1999 this sequence version replaced gi:4263152.	* NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.	* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.	1	13925: contig of 13925 bp in length	13926	13934: gap of unknown length	13935	16026: contig of 2092 bp in length	16027	16035: gap of unknown length	16036	81454: contig of 65419 bp in length	81455	81463: gap of unknown length	81464	161281: contig of 79818 bp in length	161290	161290: gap of unknown length	161291	163945: contig of 2655 bp in length	163946	163954: gap of unknown length	163955	167128: contig of 3174 bp in length	167129	167137: gap of unknown length	167138	202845: contig of 35708 bp in length	202846	202854: gap of unknown length	202855	205084: contig of 2230 bp in length	205085	205093: gap of unknown length	205094	209517: contig of 4424 bp in length	209518	209526: gap of unknown length	209527	221793: contig of 12267 bp in length	221794	221802: gap of unknown length	221803	228079: contig of 6277 bp in length	228080	228088: gap of unknown length	228089	231641: contig of 3553 bp in length	231642	231649: gap of unknown length	231650	262336: contig of 30687 bp in length.
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	Best Local Similarity	79.5%;	Pred. No. 8e-17;	49;	Indels	8;	Gaps	4																																															
	Matches	221;	Conservative	0;																																																			

(GB:X17077): contains similarity to Pfam domain PF00046 (homeobox). Score=93.6, E-value=1.3e-24, N=1; coded for by the following C. elegans cDNAs: YK466g11.3, YK466g11.5, YK678b7.3, YK678b7.5, X17077"

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/note="for a graphical representation of this gene see:

Query Match 2.2%; Score 143.4; DB 3; Length 56448;
Best Local Similarity 66.6%; Pred. No. 1e-16;
Matches 233; Conservative 0; Mismatches 108; Indels 9; Gaps 2;

CDS

DB 4677 ACACGAAATTTTGCATTTTGCATTTTAAATFAGCATACCTGCTGACACGAAATAT 4736
ACCGGAAATTTTGCATTTTGCATTTTAAATFAGCATACCTGCTGACACGAAATAT 4736
DB 36924 ACACGAAATTTTGCATTTTGCATTTTAAATFAGCATACCTGCTGACACGAAATAT 36983
ACCGGAAATTTTGCATTTTGCATTTTAAATFAGCATACCTGCTGACACGAAATAT 36983
DB 4737 TTTGTTAAATTTGCAAAAGTGTGCGCTTTAAGAGTCTGATTTGAACCTTGTG 4796
TTTTGTTAAATTTGCAAAAGTGTGCGCTTTAAGAGTCTGATTTGAACCTTGTG 4796
DB 36984 TTTGTTAAATTTGCAAAAGTGTGCGCTTTAAGAGTCTGATTTGAACCTTGTG 37043
TTTTGTTAAATTTGCAAAAGTGTGCGCTTTAAGAGTCTGATTTGAACCTTGTG 37043
DB 4797 TTGCGACTTTTCATGATTTTTCGTAGCGTTTTCATGAGAAATATGATTTAT 4856
TTTTCGTAGCGTTTTCATGATTTTTCGTAGCGTTTTCATGAGAAATATGATTTAT 4856
DB 37044 ATGTGGAAATTTTATGATTTTTCATGATTTTTCATGATTTTTCATGATTTT 37101
ATGTGGAAATTTTATGATTTTTCATGATTTTTCATGATTTTTCATGATTTT 37101
DB 4857 TCAAAATTTATTTTACGATTCGGAAGAAACAAATGAGAACCGATTAATATC 4916
TCAAAATTTATTTTACGATTCGGAAGAAACAAATGAGAACCGATTAATATC 4916
DB 37102 TCA-----CTTTTAACTAATAATTAATTTGTTGAGAAATTTGAAATAATCGGC 37154
TCA-----CTTTTAACTAATAATTAATTTGTTGAGAAATTTGAAATAATCGGC 37154
DB 4917 GCAGCAACATAGTTGAATTAACATGATCTTTTAAGGNGNCATTTCCATATTTTC 4976
GCAGCAACATAGTTGAATTAACATGATCTTTTAAGGNGNCATTTCCATATTTTC 4976
DB 37155 GCAGCAACGAAATTTGAATTAACATGATCTTTTAAAGCATATCCGTTTCGATTTAA 37214
GCAGCAACGAAATTTGAATTAACATGATCTTTTAAAGCATATCCGTTTCGATTTAA 37214
DB 4977 ACACAACTTGTGTCGTCGNNCGGTTTCGTCATTTTGAAGCAAAAT 5026
ACACAACTTGTGTCGTCGNNCGGTTTCGTCATTTTGAAGCAAAAT 5026
DB 37215 CAACACACTGTGTCGTCGACGACGCGTACCGTATTTTCGCGCAAAAT 37264
CAACACACTGTGTCGTCGACGACGCGTACCGTATTTTCGCGCAAAAT 37264

RESULT 14

DB 023139 37794 bp DNA linear INV 22-MAY-2002
023139
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Pelodetinae; Caenorhabditis.
1 (bases 1 to 37794)
Waterson, R.
Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
Science 282 (5396), 2012-2018 (1998)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

99069613
851916
2 (bases 1 to 37794)
Ding H.
The sequence of C. elegans cosmid F13H8
unpublished (2001)
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS
REFERENCE

Submitted (13-JUL-1995)
4 (bases 1 to 37794)
Waterson, R.
Direct Submission
Submitted (11-APR-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 37794)
Waterson, R.
Direct Submission
Submitted (14-SEP-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
6 (bases 1 to 37794)

AUTHORS
TITLE
JOURNAL

COMMENT

Waterston, R.
Direct Submission
Submitted (22-MAY-2002) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 1RQ, England
email: rwenematecode.wustl.edu and jess@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.
It may be shorter because we only sequence overlapping sections
once, or longer because we provide a small overlap between
neighboring submissions.

This sequence was finished as follows unless otherwise noted: all
regions were double stranded, sequenced with an alternate chemistry
or covered by high quality data (i.e., phred quality >= 30); an
attempt was made to resolve all sequencing problems, such as
compressions and repeats: all regions were covered by sequence from
more than one m13 subclone.

For a graphical representation of this cosmid sequence and its
analysis see:
http://www.wormbase.org/db/seq/sequence?name=F13H8;class=Sequence

NEIGHBORING COSMID INFORMATION

The 5' cosmid is T24H7, 300 bp overlap; the 3' cosmid is C29F5, 200
bp overlap. Actual start of this cosmid is at base position 297 of
F13H8; actual end is at 37794 of F13H8.

NOTES:

Coding sequences below are the result of integration and manual
review of the following data: computer analysis using the program
GeneFinder (P. Green and L. Hillier, personal communication), the
large scale EST projects of Yuji Kohara
(http://www.ddb.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C.
elegans ORFome cloning project (http://wormfdb.fci.harvard.edu/),
(http://blast.wustl.edu/) sequence conservation with C. briggsae
using Jim Kent's WABA alignment program (Genome Research
10:1115-1125, 2000), individual C. elegans GenBank submissions,
and personal communications with C. elegans researchers. tRNAs
are predicted using the program tRNAscan-SE (Lowe, T.M. and
Eddy, S.R., 1997, Nucleic Acids Res., 25, 955-964).

FEATURES

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1. 37794
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/chromosome="I"
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gene

CDS

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/protein_id="AAK31493.1"
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/translation="MIRFVATVAITLANAHCOYWPEDHOQFNNGFPOFOQOOF

gene

CDS

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/db_xref="GI:15617782"

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EQALKLASTLKKRLGRETSDTWKFNHFLGNDLNCINNETTGFETGKGLHSLAT
LIGTNVKKVFNIMPIINVKIISOAKHLKFCFESHRKSCSCFELNEKEYONIKOF
DEQNLNEVQEQNFQKNGSSSTFAVIAIPADLDKSIPLKKNPIMGIALDPCFLSPIAH
DIAKQIMKGLFEPIDOKTITNLSVGFPRFCPCPECPYELRTIONSECEPSRMR
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gene

CDS

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gene

CDS

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GNAKRVLEIGHRIYEHRRPGADRNKSNANGKDVRLPEKELOSTGYSDSRANVSMR
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/note="Contains similarity to Pfam domain: PF01156
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for by the following C. elegans cDNAs: YK119d3.3,
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/codon_start=1
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/protein_id="AAK31485.1"
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VFIAQDSLIVKRPGLIOWEELFGSDIGIGVDEPKLPPDSNQAQVGNVADINLT
KSTQDILVIGLPLTNIAAIRKPDQISKGVKQVYIMGVYLGVMQFNSTAEFNL
MDPAAHIVLSLHTTMIIPMDTCFLKPEVNEVDYDESNQTKTSLSTNTTANGR
QYKASGOIYAFVDDIVASVADIPRIAVRMNTLCSSVELKELVAVAGQVTDVMLTKY
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AV" complement(12821. .14697)
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Best Local Similarity	64.0%;	Pred. No. 1.5e-10;							
Matches	260;	Conservative	0;	Mismatches	136;	Indels	10;	Gaps	3

Matches	260;	Conservative	0;	Mismatches	136;	Indels	10;	Gaps	2
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OY	4639	GTTTGTGAATTCCTTAATTAGTAGAGCTTTATAAAGCTTATTTATTAACAATAAAGG	839
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OY	4699	ACGTTAAATACGATCACCTGGTGTCGCACACGAACAATTTTT-GTTAAATCAAAAAGTG	4757
Db	840	CGCCAAAAAATACGGTATCCGGTCTGCACACGAATAATTTTATTTAAATGCAAAATAGTG	899
OY	4758	TGGCGCCTTAAAGAGCGGTACTTTGAACACTCGTTGGCGCATTTTCATCGATT	4817
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OY	4818	TTGCGACCTTTTATTTATAAGAAAAATGATTTATTTATTCAAAAATTTATTTAACGA	4877
Db	960	TTTATATCTATTTTATAAATTTATATGTAATTTTGTGATAACAAAAATATTTTGTGCA	1019
OY	4878	ATCCGCAAAAACAAATGAAGAACCACCGATAAAAATATCGCAGACAACATATTTGGAAAT	4937
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Db	1131	ACCGGATATCGTAATTTTGAACGCAAAATGCAAACTTTGCATCTA	1176

RESULT 15				
AC006760				
LOCUS	AC006760	309026 bp	DNA	linear
DEFINITION	Caenorhabditis elegans clone Y41D4, ***	SEQUENCING	IN PROGRESS	***
	21 unoriented pieces.			

ACCESSION	AC006760
VERSION	AC006760.2
KEYWORDS	HTGS_PHASE1.
SOURCE	Caenorhabditis elegans
ORGANISM	Caenorhabditis elegans

REFERENCE
1 (bases 1 to 309026)
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis

AUTHORS Waterston, R.H.
TITLE The sequence of *Caenorhabditis elegans* clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 309026)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis

COMMENT

MO 63108 USA
On Mar 1, 1999 this sequence version replaced gi:4263178.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved. 3227: contig of 2327 bp in length
1

*	2328	2336:	gap of unknown length
*	2337	27261:	contig of 24925 bp in length
*	27262	27270:	gap of unknown length
*	27271	29305:	contig of 2035 bp in length
*	29306	29314:	gap of unknown length
*	29315	31657:	contig of 2243 bp in length
*	31658	31666:	gap of unknown length
*	31667	34340:	contig of 2674 bp in length
*	34341	34349:	gap of unknown length
*	34350	37935:	contig of 3586 bp in length
*	37936	37944:	gap of unknown length
*	37945	41236:	contig of 3282 bp in length
*	41237	41245:	gap of unknown length
*	41246	62684:	contig of 21439 bp in length
*	62685	62693:	gap of unknown length
*	62694	100030:	contig of 37337 bp in length
*	100031	100039:	gap of unknown length
*	100040	108178:	contig of 8139 bp in length
*	108179	108187:	gap of unknown length
*	108188	122341:	contig of 14154 bp in length
*	122342	122350:	gap of unknown length
*	122351	124992:	contig of 2642 bp in length
*	124993	125001:	gap of unknown length
*	125002	180556:	contig of 5555 bp in length
*	180557	180565:	gap of unknown length
*	180566	217370:	contig of 36805 bp in length
*	217371	217378:	gap of unknown length
*	217379	220465:	contig of 3087 bp in length
*	220466	220473:	gap of unknown length
*	220474	266237:	contig of 47764 bp in length
*	266238	266245:	gap of unknown length
*	268238	268246:	gap of unknown length
*	268246	285323:	contig of 15270 bp in length
*	283516	285323:	gap of unknown length
*	283524	291601:	contig of 8078 bp in length
*	291602	291609:	gap of unknown length
*	291610	295697:	contig of 4088 bp in length
*	295698	295705:	gap of unknown length
*	295706	297760:	contig of 2055 bp in length
*	297761	297766:	gap of unknown length
*	297769	309026:	contig of 11288 bp in length.

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FEATURES
source      location/Qualifiers
1. . 309026 1. . 309026
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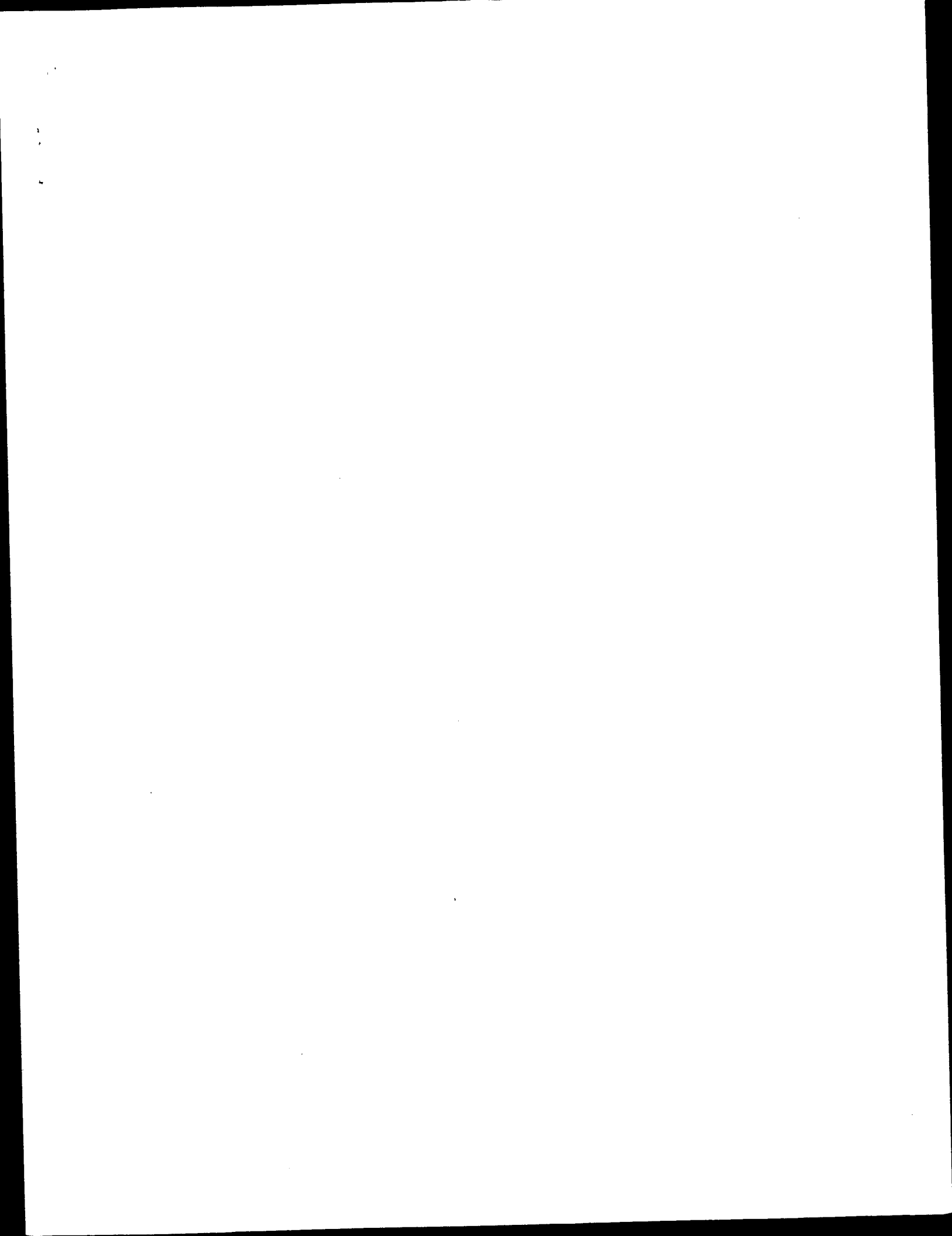
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Query Match	2.2%;	Score 142.6;	DB 2;	Length 309026;
Best Local Similarity	62.9%;	Pred. No. 1.2e-16;		
Matches 273;	Conservative	0;	Mismatches 138;	Indels 23;
				Gaps 3

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Db	200189	TTTATTTTCAATTAAGATTTTATCAATCTCCGTAATCAAAATTTTCGATTTTGAGT	2002
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Db	200249	GAAATACGGTACCCGTTCTCGACAGGCA-ATTTTAAAAACAACAAAAGCTGTGTC	2003
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Db 200428 ATATTAATAAAAAAACTCTAAATTTTAAATGATTAATGAAAAATCGATAAATAATTCGCGAG 200487
QY 4921 CACCATATGTTGAAATTTACAGTACTCTTTTAAAGNNCCACATTTCTATATTATACAC 4980
Db 200488 CACCAAAATTTTAAATATACAGTACTTTAAAGGGGAGACCCCNITGTTATTATACCG 200547
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Db 200548 AAAATTCACCGGTGAGACCGCATACCGTATTTTCGGCGCAAAAAATCCCAATTTTAAAC 200607
QY 5041 ATATGTTCAAAAAA 5054
Db 200608 GTCTGGGTAATATA 200621

Search completed: February 28, 2003, 03:13:57
Job time : 21158.4 secs



GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 19:36:05 ; Search time 200.757 Seconds
(without alignments)
10021.077 Million cell updates/sec

Title: US-09-993-420a-1

Perfect score: 6560

Sequence: 1 atcgatagcgcgcaccacaat.....gtttgtaataaataatca 6560

Scoring table: IDENTITY_NUC

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

- Issued_Patents_NA:*
- 1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/lna/PCTUS.COMB.seq:*
- 6: /cgn2_6/ptodata/1/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6541.8	99.7	6560	5	PCT-US93-05651-1
2	6529.8	99.5	6559	4	US-09-234-186-1
3	6529.8	99.5	6559	4	US-09-233-527-1
4	632.6	9.6	1315	4	US-09-234-186-2
5	632.6	9.6	1315	4	US-09-234-186-4
6	632.6	9.6	1315	4	US-09-234-186-5
7	632.6	9.6	1315	4	US-09-234-186-6
8	632.6	9.6	1315	4	US-09-233-527-2
9	632.6	9.6	1315	4	US-09-233-527-4
10	632.6	9.6	1315	4	US-09-233-527-5
11	632.6	9.6	1315	4	US-09-233-527-6
12	632.6	9.6	1315	5	PCT-US93-05651-2
13	139.2	2.1	7653	3	US-08-394-189B-1
14	139.2	2.1	7653	3	US-08-258-287B-1
15	139.2	2.1	7653	3	US-08-368-704C-1
16	139.2	2.1	7653	5	PCT-US93-05701-18
17	139.2	2.1	7653	5	PCT-US93-05701-18
18	122.8	1.9	6559	4	PCT-US93-05705-1
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22	101.8	1.6	7653	3	US-08-258-287B-1
23	101.8	1.6	7653	3	US-08-368-704C-1
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27	82.4	1.3	132	3	US-08-368-704C-7

28	81.8	1.2	7218	1	US-08-233-463-14	Sequence 14, Appl
29	80.2	1.2	111	3	US-08-258-287B-8	Sequence 8, Appl1
30	80.2	1.2	111	3	US-08-368-704C-8	Sequence 8, Appl1
31	79.4	1.2	114	3	US-08-258-287B-21	Sequence 21, Appl
32	79.4	1.2	114	3	US-08-368-704C-21	Sequence 21, Appl
33	77.6	1.2	6840	4	US-08-980-241-8	Sequence 8, Appl1
34	77.2	1.2	132	3	US-08-258-287B-3	Sequence 3, Appl1
35	77.2	1.2	132	3	US-08-368-704C-3	Sequence 3, Appl1
36	76.6	1.2	122	3	US-08-258-287B-9	Sequence 9, Appl1
37	76.6	1.2	122	3	US-08-368-704C-9	Sequence 9, Appl1
38	70.2	1.1	116	3	US-08-258-287B-5	Sequence 5, Appl1
39	70.2	1.1	116	3	US-08-368-704C-5	Sequence 5, Appl1
40	68.6	1.0	29793	4	US-09-511-477-38	Sequence 38, Appl
41	68.6	1.0	29793	4	US-09-511-507-38	Sequence 38, Appl
42	68.6	1.0	29793	4	US-09-511-507-38	Sequence 38, Appl
43	65.4	1.0	132	3	US-08-258-287B-3	Sequence 3, Appl1
44	65.4	1.0	132	3	US-08-368-704C-3	Sequence 3, Appl1
45	64	1.0	103	3	US-08-258-287B-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
PCT-US93-05651-1
Sequence 1, Application PC/TUS9305651
GENERAL INFORMATION:

WO 93/25683 A1

TITLE OF INVENTION: A Gene Which Prevents Programmed Cell Death
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05651
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-05651-1

Query Match 99.7%; Score 6541.8; DB 5; Length 6560;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATCGATAGTCGTCACCAATGATTTTCGATTTCTCAGTGCATGCTCACAATTTA	60
DB	1	ATCGATAGTCGTCACCAATGATTTTCGATTTCTCAGTGCATGCTCACAATTTA	60
QY	61	CAAAATCTCGAAGAAAGATGCAAGAGATGTAAGAGTTCCGAATCAATATTT	120
DB	61	CAAAATCTCGAAGAAAGATGCAAGAGATGTAAGAGTTCCGAATCAATATTT	120
QY	121	TAATTTAAATAATTCATTTGCAATTTGAAATCACTCTACTCGTTTGAATATGCA	180
DB	121	TAATTTAAATAATTCATTTGCAATTTGAAATCACTCTACTCGTTTGAATATGCA	180
QY	181	TCCTTTAAGTAACCTTGATGATGCCATTTCTCAGAAATTCCTCAAGTAGGTT	240
DB	181	TCCTTTAAGTAACCTTGATGATGCCATTTCTCAGAAATTCCTCAAGTAGGTT	240
QY	241	TGCTAGTATTTCTCCGCAAGAAATGAGACCTTCGATCTCGAGAGCGGAT	300
DB	241	TGCTAGTATTTCTCCGCAAGAAATGAGACCTTCGATCTCGAGAGCGGAT	300
QY	301	TTTATTAACAAAACCTATTCAGACCAACCATAGAGCTTTTCAATTTCTGATTTGG	360
DB	301	TTTATTAACAAAACCTATTCAGACCAACCATAGAGCTTTTCAATTTCTGATTTGG	360
QY	361	CTGTCCATTTGAGACCAACCTTTTAACGCTGTCAGCAAGATGCTCAGTCGCA	420
DB	361	CTGTCCATTTGAGACCAACCTTTTAACGCTGTCAGCAAGATGCTCAGTCGCA	420

QY 421 AGGATTAAGGCTCATTTTGAAGCGAATTTTACTAAATCTCAGCATGAGATCGAT 480
| | | | |
Db 421 AGGATTAAGGCTCATTTTGAAGCGAATTTTACTAAATCTCAGCATGAGATCGAT 480
QY 481 GGAATCAGAAATTCGAGGAATTTAGATTTTCATCTTGAAATTTGCAATGGAATAAT 540
| | | | |
Db 481 GGAATCAGAAATTCGAGGAATTTAGATTTTCATCTTGAAATTTGCAATGGAATAAT 540
QY 541 ATTCAAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAG 600
| | | | |
Db 541 ATTCAAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAG 600
QY 601 GAAATGCGCCCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
| | | | |
Db 601 GAAATGCGCCCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 ACTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
| | | | |
Db 661 ACTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 CCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
| | | | |
Db 721 CCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 ATTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
| | | | |
Db 781 ATTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 ACATCGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
| | | | |
Db 841 ACATCGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 TGTGTACGATGAGAGAAATGTATTAACAGACACATCTTTTCAATTAATTAATTA 960
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Db 901 TGTGTACGATGAGAGAAATGTATTAACAGACACATCTTTTCAATTAATTAATTA 960
QY 961 TATTCACAGTCCGAGGAAAGACGCAATCCAGAGTTGGAGTGGGAATACGTTGTAAG 1020
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Db 961 TATTCACAGTCCGAGGAAAGACGCAATCCAGAGTTGGAGTGGGAATACGTTGTAAG 1020
QY 1021 CAGGCTCCAGAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
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Db 1021 CAGGCTCCAGAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 TGTATGCTCTCCGATTCATAGAAATCAGCGGTTGTATAGCGGGAACCTCTCTGCTC 1140
| | | | |
Db 1081 TGTATGCTCTCCGATTCATAGAAATCAGCGGTTGTATAGCGGGAACCTCTCTGCTC 1140
QY 1141 GGAGGAATCGGATTCGAGTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
| | | | |
Db 1141 GGAGGAATCGGATTCGAGTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 AGCTGGAATTCACATTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
| | | | |
Db 1201 AGCTGGAATTCACATTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 ATTTTCATACCTTTAAGGAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
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Db 1261 ATTTTCATACCTTTAAGGAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 AATGTTGAGCAGGTGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1380
| | | | |
Db 1321 AATGTTGAGCAGGTGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1380
QY 1381 TTCAGATCTCAAAATCGGATATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1440
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Db 1381 TTCAGATCTCAAAATCGGATATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1440
QY 1441 TTGTCTTCACTCTTGCCGAGAACAGACAGACAGACAGACAGACAGACAGACAGACAG 1500
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Db 1441 TTGTCTTCACTCTTGCCGAGAACAGACAGACAGACAGACAGACAGACAGACAGACAG 1500

QY 1501 TTCTTTTCTTCTCTGCGCCGAGCCCTGAGCAATTCGTGCAATTTACTTTTACCGTGG 1560
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Db 1501 TTCTTTTCTTCTCTGCGCCGAGCCCTGAGCAATTCGTGCAATTTACTTTTACCGTGG 1560
QY 1561 AATTCCTGCAATTTCT 1620
| | | | |
Db 1561 AATTCCTGCAATTTCT 1620
QY 1621 GCTTAGAATGATATTTATGATATTAAGAAAGCAATTAATTAATTAATTAATTAATTA 1680
| | | | |
Db 1621 GCTTAGAATGATATTTATGATATTAAGAAAGCAATTAATTAATTAATTAATTAATTA 1680
QY 1681 GCGGCAACTGCTGAGCAATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
| | | | |
Db 1681 GCGGCAACTGCTGAGCAATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
QY 1741 AAGGATTTCTGGGATTAAGGACAGAGCCGACGATTTGGAATTCATATGATGATCT 1800
| | | | |
Db 1741 AAGGATTTCTGGGATTAAGGACAGAGCCGACGATTTGGAATTCATATGATGATCT 1800
QY 1801 CAGGATTCGCTGAGCAATTCGAGGCTGCTGAGCGGAAAGATTCATATGAGATGCA 1860
| | | | |
Db 1801 CAGGATTCGCTGAGCAATTCGAGGCTGCTGAGCGGAAAGATTCATATGAGATGCA 1860
QY 1861 ATTGATGAAAAATCATGATTTGGAGAGCCAGAGCTTGATATGAGAGATTTGTGCTA 1920
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Db 1861 ATTGATGAAAAATCATGATTTGGAGAGCCAGAGCTTGATATGAGAGATTTGTGCTA 1920
QY 1921 AATTTTAAATTTTGTGTAATTAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
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Db 1921 AATTTTAAATTTTGTGTAATTAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
QY 1981 CACCGAATCCGCAAAAGGAAATGGAATGTTGGAGACCGGAGTTCCGTGTGAGATG 2040
| | | | |
Db 1981 CACCGAATCCGCAAAAGGAAATGGAATGTTGGAGACCGGAGTTCCGTGTGAGATG 2040
QY 2041 CAACCGGAGCAGCAATGATGCGAATTTAGGAACGATTCAGAGAAAGCAGCGGAA 2100
| | | | |
Db 2041 CAACCGGAGCAGCAATGATGCGAATTTAGGAACGATTCAGAGAAAGCAGCGGAA 2100
QY 2101 AATTTGAGACCTTCTGTGAGCAGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTG 2160
| | | | |
Db 2101 AATTTGAGACCTTCTGTGAGCAGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTG 2160
QY 2161 CAGGATGCTGCTGCGAGCTTGGAAATGCAAGACAGATCAATGCTGCTGATGGA 2220
| | | | |
Db 2161 CAGGATGCTGCTGCGAGCTTGGAAATGCAAGACAGATCAATGCTGCTGATGGA 2220
QY 2221 CGTTGCTAAGGAGAAATGCTGAAATTTGCAAAATTTGCAAAATTTGCAAAATTTG 2280
| | | | |
Db 2221 CGTTGCTAAGGAGAAATGCTGAAATTTGCAAAATTTGCAAAATTTGCAAAATTTG 2280
QY 2281 AGGTGCGAGAAAAATGCTGCAAAATTTGTTGTTTCTTCAAGAAATTCAGAAATTC 2340
| | | | |
Db 2281 AGGTGCGAGAAAAATGCTGCAAAATTTGTTGTTTCTTCAAGAAATTCAGAAATTC 2340
QY 2341 TGTGCAAAATTTAGCCCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
| | | | |
Db 2341 TGTGCAAAATTTAGCCCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
QY 2401 TTTTGTATCCGGAATTTGATTTTGTGATTAATTTAGCAAAATTTGCAAAATTTG 2460
| | | | |
Db 2401 TTTTGTATCCGGAATTTGATTTTGTGATTAATTTAGCAAAATTTGCAAAATTTG 2460
QY 2461 ATTAAAAACGTTATTTTCTATTCGAATTTTAAAGCATATTTCTGATTTGATTT 2520
| | | | |
Db 2461 ATTAAAAACGTTATTTTCTATTCGAATTTTAAAGCATATTTCTGATTTGATTT 2520
QY 2521 GCGAAAAAGATCTGCTATTTATCAAAATTCGCTTTTAAATTTTAAATTTTAAATTT 2580
| | | | |
Db 2521 GCGAAAAAGATCTGCTATTTATCAAAATTCGCTTTTAAATTTTAAATTTTAAATTT 2580
QY 2581 ACATTAATTCGATTTTGAACCTTTTCTTGAAAAAACAGGTTTCTGCTGATTTGC 2640
| | | | |

D	2581	ACATTAAATGATTTTGAACCTTTTCTCGAAAAACAGTGTTCGTGATTTGC	2640	D	3661	ACTGGAAGAGTGGGAAAGCTAGGCCAACAAATTACGGCTCTGTGTGATTAACGATTT	3720
Q	2641	TGAACGAAAAACCCCAAAATTCATTTTCGAACATTTAAACCCGAAAAATCGTTTTT	2700	Q	3721	TACTGCAATTTTTCCGATTTGCTTTTTTTTGGCCAAACCTACTTCCCGTAATATCA	3780
D	2641	TGACGAAAAAACCCCAAAATTCATTTTCGAACATTTAAACCCGAAAAATCGTTTTT	2700	D	3721	TACTGCAATTTTTCCGATTTGCTTTTTTTTGGCCAAACCTACTTCCCGTAATATCA	3780
Q	2701	TAACTTAATTTTCCGCCGAAATGACGAATTAATTTGCAAAATTTCTAATTTTCAGATA	2760	Q	3781	ACTTTCCGTCGTGTGATTAATTTTTCGATTTTGTGTAACAAACCTTAACCTTTTTCGCGCTG	3840
D	2701	TAACTTAATTTTCCGCCGAAATGACGAATTAATTTGCAAAATTTCTAATTTTCAGATA	2760	D	3781	ACTTTCCGTCGTGTGATTAATTTTTCGATTTTGTGTAACAAACCTTAACCTTTTTCGCGCTG	3840
Q	2761	GGCTTAATCTGCTGGGGGCTTCTGAGTGCAGAAAAATGATGGAATCCGTGGAACCTGCAG	2820	Q	3841	GCCTAGCCTCCGCTCTCTCCACATTTCCAAAGTACCCCTGTATCTCAATTAATTCATC	3900
D	2761	GGCTTAATCTGCTGGGGGCTTCTGAGTGCAGAAAAATGATGGAATCCGTGGAACCTGCAG	2820	D	3841	GCCTAGCCTCCGCTCTCTCCACATTTCCAAAGTACCCCTGTATCTCAATTAATTCATC	3900
Q	2821	GGACAAAGTGCAGAAACCTCTGCTTACACATGCTGTTCAACAAAGCGGATCCGCAC	2880	Q	3901	TTCACTTTAACTGTCTCTTTTGTGAGCCCTTTCGAACTCCGCCAAATTCCTGTACGC	3960
D	2821	GGACAAAGTGCAGAAACCTCTGCTTACACATGCTGTTCAACAAAGCGGATCCGCAC	2880	D	3901	TTCACTTTAACTGTCTCTTTTGTGAGCCCTTTCGAACTCCGCCAAATTCCTGTACGC	3960
Q	2881	AACTGGAAGGAACACAAATCGAGCTGGGTAAAGAGTATTTGCATAGACATTAGAAGTCAA	2940	Q	3961	GTACGCGACTTTGATTTATTTTTCATTTTTCGAAATTTTCTCTACAAACAAAAAAC	4020
D	2881	AACTGGAAGGAACACAAATCGAGCTGGGTAAAGAGTATTTGCATAGACATTAGAAGTCAA	2940	D	3961	GTACGCGACTTTGATTTATTTTTCATTTTTCGAAATTTTCTCTACAAACAAAAAAC	4020
Q	2941	TATCCCTTTCCCTAGTACCTTACCTTCCCGGGGTGTGTGTAAGCCGATTAATTAACAG	3000	Q	4021	GGTCTTTTATTCACCCCTTTTTCGGAACGAACCTGCAATTTTGAATAGGCGTGGC	4080
D	2941	TATCCCTTTCCCTAGTACCTTACCTTCCCGGGGTGTGTGTAAGCCGATTAATTAACAG	3000	D	4021	GGTCTTTTATTCACCCCTTTTTCGGAACGAACCTGCAATTTTGAATAGGCGTGGC	4080
Q	3001	GTTGGTAGCCTCTTGGGGGGACAGCTGGAACATATTCAGTATTAATTAATTAATTAAT	3060	Q	4081	AAAGAAATCCGGTTTTCATTTTTCGCAATCGTATCCAAAAAGTTTATAGTGAATAAT	4140
D	3001	GTTGGTAGCCTCTTGGGGGGACAGCTGGAACATATTCAGTATTAATTAATTAATTAAT	3060	D	4081	AAAGAAATCCGGTTTTCATTTTTCGCAATCGTATCCAAAAAGTTTATAGTGAATAAT	4140
Q	3061	AATGTTATTTGAGGGGATACAAATTTGCAGAAATGCTATTTTTCACAAATTTTGAAGC	3120	Q	4141	TCATTTTAAATTAATTAATTAATTTTCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT	4200
D	3061	AATGTTATTTGAGGGGATACAAATTTGCAGAAATGCTATTTTTCACAAATTTTGAAGC	3120	D	4141	TCATTTTAAATTAATTAATTAATTTTCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT	4200
Q	3121	GCAAAATTTCCAGTAGAGAAACTACAGTATTTCTTAATTTTAAATTTTAAATTTTAACT	3180	Q	4201	TCGATGGCTTGTGATTTTTCGAAACAAATTTTGTAGTGAATAGCATCCGCC	4260
D	3121	GCAAAATTTCCAGTAGAGAAACTACAGTATTTCTTAATTTTAAATTTTAAATTTTAACT	3180	D	4201	TCGATGGCTTGTGATTTTTCGAAACAAATTTTGTAGTGAATAGCATCCGCC	4260
Q	3181	AAAGAAATTAACACTAATCAAAAATTAATTTCAAAAATCGAGCCGTAATTCAGCT	3240	Q	4261	GCCTTATGCTGTTTACCATCAGATAGGCTCCGCCATTTGATTCCTTGAATTTTGTG	4320
D	3181	AAAGAAATTAACACTAATCAAAAATTAATTTCAAAAATCGAGCCGTAATTCAGCT	3240	D	4261	GCCTTATGCTGTTTACCATCAGATAGGCTCCGCCATTTGATTCCTTGAATTTTGTG	4320
Q	3241	ACAGTAGCATTAAAGAAATTAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3300	Q	4321	GTATTAATAACAAAAACCTTATAGTACGATTCGCAAAAACCAATGGTGTATTAAT	4380
D	3241	ACAGTAGCATTAAAGAAATTAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3300	D	4321	GTATTAATAACAAAAACCTTATAGTACGATTCGCAAAAACCAATGGTGTATTAAT	4380
Q	3301	GTTGTGAATTAACGATTCAGGATTTTGTGTTCCCGGAAATGCTCTAAAGCATTTAT	3360	Q	4381	TCACCTCTGTTGTTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT	4440
D	3301	GTTGTGAATTAACGATTCAGGATTTTGTGTTCCCGGAAATGCTCTAAAGCATTTAT	3360	D	4381	TCACCTCTGTTGTTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT	4440
Q	3361	TGTGAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	3420	Q	4441	TCGAAGGTACACTAATTTTGTATTAAGAGAGATTCAGAGAGAGTACCTTTGGGAGAA	4500
D	3361	TGTGAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	3420	D	4441	TCGAAGGTACACTAATTTTGTATTAAGAGAGATTCAGAGAGAGTACCTTTGGGAGAA	4500
Q	3421	ATGAAGAAGAGACTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3480	Q	4501	ACATACCTGAGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT	4560
D	3421	ATGAAGAAGAGACTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3480	D	4501	ACATACCTGAGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT	4560
Q	3481	CGGTGCTGATTTGCGCTGAGTACAGCTGAGCCATTGGAAATGCTTGGAGTCTGTC	3540	Q	4561	CCTAAATAATGAAGTTTTCACCTGTTTTCAAAGAAAGCCGAATTCGACAGCTTTAC	4620
D	3481	CGGTGCTGATTTGCGCTGAGTACAGCTGAGCCATTGGAAATGCTTGGAGTCTGTC	3540	D	4561	CCTAAATAATGAAGTTTTCACCTGTTTTCAAAGAAAGCCGAATTCGACAGCTTTAC	4620
Q	3541	GCTGTGGGGGAGTGTTCAGCTGAGTACGATTAATTTTGTAAATTAATTAATTAAT	3600	Q	4621	GAGATTTTCAATTAATTTTGTATTTGAATTTTCAATTTTCAATTTTCAATTTTCAAT	4680
D	3541	GCTGTGGGGGAGTGTTCAGCTGAGTACGATTAATTTTGTAAATTAATTAATTAATTAAT	3600	D	4621	GAGATTTTCAATTAATTTTGTATTTGAATTTTCAATTTTCAATTTTCAATTTTCAAT	4680
Q	3601	TTATGTACAACTCTTACATTTTGTAAATTTTGTAAATTTTGTAAATTTTGTAAAT	3660	Q	4681	GAAATTTTGCATTTTGTAGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT	4740
D	3601	TTATGTACAACTCTTACATTTTGTAAATTTTGTAAATTTTGTAAATTTTGTAAAT	3660	D	4681	GAAATTTTGCATTTTGTAGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT	4740
Q	3661	ACTGGAAGAGTGGGAAAGCTAGGCCAACAAATTACGGCTCTGTGTGATTAACGATTT	3720	Q	4741	TTAAATTCAAAAAGATGTGCGCTTTTAAAGAGTGTGCTGATTTGAACCTTCTGTGTC	4800
D	3661	ACTGGAAGAGTGGGAAAGCTAGGCCAACAAATTACGGCTCTGTGTGATTAACGATTT	3720	D	4741	TTAAATTCAAAAAGATGTGCGCTTTTAAAGAGTGTGCTGATTTGAACCTTCTGTGTC	4800

QY 4801 GGACTTTTCATCGATTTTTCGATGCGTTTATATAGAAAAATGTATTTATTTTCAA 4860
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Db 4801 GGACTTTTCATCGATTTTTCGATGCGTTTATATAGAAAAATGTATTTATTTCAA 4860
QY 4861 AAATTTATTTTACCGGATTCGGAAAAAATGAAGAACCGATTAATATTCGAG 4920
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Db 4861 AAATTTATTTTACCGGATTCGGAAAAAATGAAGAACCGATTAATATTCGAG 4920
QY 4921 CAACAATAGTTTGAATTTACACTCTTTTAAAGNGNNACATTTCTATATTTTCACAC 4980
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Db 4921 CAACAATAGTTTGAATTTACACTCTTTTAAAGNGNNACATTTCTATATTTTCACAC 4980
QY 4981 AAACCTTGCTGCGNNNGGGTATCGTATTTTGAATGAGAAATTCAGAAATTCGAG 5040
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Db 4981 AAACCTTGCTGCGNNNGGGTATCGTATTTTGAATGAGAAATTCAGAAATTCGAG 5040
QY 5041 AATATGTTCAAAAACCAATTAAGGCAATTTCAAGCTTGAAGCAAAATTCAGAAAT 5100
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Db 5041 AATATGTTCAAAAACCAATTAAGGCAATTTCAAGCTTGAAGCAAAATTCAGAAAT 5100
QY 5101 TCTAAAAATTTAAAAAAATTCATTCGAAATGTGAATTTGATATTCACCTGAGTCCAT 5160
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QY 5161 ATGGCAAAATTTGCTATTCGCGNNNTTCGANNATTTTGTTCACGCGGCGGAAAAAG 5220
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Db 5161 ATGGCAAAATTTGCTATTCGCGNNNTTCGANNATTTTGTTCACGCGGCGGAAAAAG 5220
QY 5221 AAGCAGCAATTTGATTTCTGCAATTTTCTGACGCTGTCATTTATTTGAAACTC 5280
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Db 5221 AAGCAGCAATTTGATTTCTGCAATTTTCTGACGCTGTCATTTATTTGAAACTC 5280
QY 5281 TAATTAAGCTGATTTTCTGCTATTTGACAACTAATTCATATTTTGAATTTAA 5340
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Db 5281 TAATTAAGCTGATTTTCTGCTATTTGACAACTAATTCATATTTTGAATTTAA 5340
QY 5341 TATTAAGCTGATTTTCTGCTATTTGACAACTAATTCATATTTTGAATTTAA 5400
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Db 5341 TATTAAGCTGATTTTCTGCTATTTGACAACTAATTCATATTTTGAATTTAA 5400
QY 5401 TGCCAAATATTTCTAGAGATATTAATAAAACCTTAATTTCTGCAACACCTACAGC 5460
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Db 5401 TGCCAAATATTTCTAGAGATATTAATAAAACCTTAATTTCTGCAACACCTACAGC 5460
QY 5461 TATCAAAACGTAATTTAGTATTCATTTTCCAGTCCAGCCCGATGCAAGCTCGCTCAA 5520
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QY 5521 TGCATATGCAACAAAGAGAGAGTTCTCACTTACCGGATCCGAGACGATACCTCAA 5580
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Db 5521 TGCATATGCAACAAAGAGAGAGTTCTCACTTACCGGATCCGAGACGATACCTCAA 5580
QY 5581 TCTCTCATATCTTCATATCAACCCACATGCAACGTAAGAAAGCCGATGCAAGCTG 5640
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Db 5581 TCTCTCATATCTTCATATCAACCCACATGCAACGTAAGAAAGCCGATGCAAGCTG 5640
QY 5641 TTTCAAGATATTTGATTTCCAAAGAGATGCGTGAACCTATGATGATGATGATGCA 5700
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Db 5641 TTTCAAGATATTTGATTTCCAAAGAGATGCGTGAACCTATGATGATGATGATGCA 5700
QY 5701 CTCTTGATATTTCTTCCGCTAAAGCAAGAGAGTCTAAGAAATGTTTTTTTGT 5760
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Db 5701 CTCTTGATATTTCTTCCGCTAAAGCAAGAGAGTCTAAGAAATGTTTTTTTGT 5760
QY 5761 GGTTCGCTTTGTTGGAAGGAGACTTTCTATCTTTTATTCACCAATTAATCTATG 5820
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Db 5761 GGTTCGCTTTGTTGGAAGGAGACTTTCTATCTTTTATTCACCAATTAATCTATG 5820
QY 5821 GAAAAACGTTGAATTTTAACTGAACTGATGAGAAAAATGCGGATATGATGACAA 5880
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Db 5821 GAAAAACGTTGAATTTTAACTGAACTGATGAGAAAAATGCGGATATGATGACAA 5880

QY 5881 TTTGCCAAGTATATCTTTGNGATATACATATAAAGAGTCAAGCAATATTTAG 5940
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Db 5881 TTTGCCAAGTATATCTTTGNGATATACATATAAAGAGTCAAGCAATATTTAG 5940
QY 5941 GAAACCAAAATTAATGAGATTCGCAACATTTTACCGCAAAATATTCGAGGAA 6000
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Db 5941 GAAACCAAAATTAATGAGATTCGCAACATTTTACCGCAAAATATTCGAGGAA 6000
QY 6001 CTACAGTATTTCTTCAAAAGACTACTGTAGCGCTGTGCGATTTTACGAGCTGATTTTG 6060
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Db 6001 CTACAGTATTTCTTCAAAAGACTACTGTAGCGCTGTGCGATTTTACGAGCTGATTTTG 6060
QY 6061 AAATGAATCAGACTAGAGAAAGAGAGAAATTTGAACTATTAATGAAATCAATTCOA 6120
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Db 6061 AAATGAATCAGACTAGAGAAAGAGAGAAATTTGAACTATTAATGAAATCAATTCOA 6120
QY 6121 AAAAGTGAACCCCTGACTCAGTACGATCTTCAAGATTTAGTATTTTCTGCTACGAG 6180
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Db 6121 AAAAGTGAACCCCTGACTCAGTACGATCTTCAAGATTTAGTATTTTCTGCTACGAG 6180
QY 6181 AATTTTNGNGTCAATATGTTGNGCAATAGCAGATTCAGATTTGTCTCTGTA 6240
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Db 6181 AATTTTNGNGTCAATATGTTGNGCAATAGCAGATTCAGATTTGTCTCTGTA 6240
QY 6241 TGTCTGAAAAATTTTCCATTTCAACATCAATATAGCAATCTAAAAATGCGGTTCTGCA 6300
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Db 6241 TGTCTGAAAAATTTTCCATTTCAACATCAATATAGCAATCTAAAAATGCGGTTCTGCA 6300
QY 6301 GCGACACATATGACGTGATGCTGCAAGACCCAGTCAAGAAATCTAGCTTCTTTAAA 6360
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Db 6301 GCGACACATATGACGTGATGCTGCAAGACCCAGTCAAGAAATCTAGCTTCTTTAAA 6360
QY 6361 CAATATCAATTTTAAATTTAGTATGATTAATAATGTTGGCTACAGTACGCTGCT 6420
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Db 6361 CAATATCAATTTTAAATTTAGTATGATTAATAATGTTGGCTACAGTACGCTGCT 6420
QY 6421 TTTCAAGTCAAACTCTTAATTTAATGCGGCTTCAAAAAGTGTCTTTGAAAA 6480
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Db 6421 TTTCAAGTCAAACTCTTAATTTAATGCGGCTTCAAAAAGTGTCTTTGAAAA 6480
QY 6481 TATTAAGCTTATATTTATTTATTAATAAATTTGATATCATATCAAAAGCAGTA 6540
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Db 6481 TATTAAGCTTATATTTATTTATTAATAAATTTGATATCATATCAAAAGCAGTA 6540
QY 6541 GTTGTATTAATAATTTATCA 6560
|||||
Db 6541 GTTGTATTAATAATTTATCA 6560

RESULT 2
US-09-234-186-1
; Sequence 1, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Hengartner, Michael
; APPLICANT: Horvitz, H. Robert
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; EARLIER FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

; LENGTH: 6559
 ; TYPE: DNA
 ; ORGANISM: Caenorhabditis elegans
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(6559)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-234-186-1

Query Match 99.5%; Score 6529.8; DB 4; Length 6559;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 6559; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATCGATAGTCTGACCAATGATTTTCGATTTCTCATGTCATGCGGCACAAATTTA 60
 Db 1 ATCGATAGTCTGACCAATGATTTTCGATTTCTCATGTCATGCGGCACAAATTTA 60
 QY 61 CAAATCTCGAGAAAAGAAAGATGCAAGATATGAAGAGTTCCGAAATCTAAATATT 120
 Db 61 CAAATCTCGAGAAAAGAAAGATGCAAGATATGAAGAGTTCCGAAATCTAAATATT 120
 QY 121 TAATTTAAAAAATCAATTTGAAATTTCAACTCTCTGCTTTTGAATAATGCCAA 180
 Db 121 TAATTTAAAAAATCAATTTGAAATTTCAACTCTCTGCTTTTGAATAATGCCAA 180
 QY 181 TCCCTTAAGTAACTTTGATGCGCCATTTCTTCAGAAATTCCTTCAAAAGTAGTGT 240
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QY 2161 CAGATGATGTTGCGAGGTTGGAATGACAGACAGATCAATGCTCATGTTATGGA 2220
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Qy 6541 GTTGTATATAAATATATCA 6560
Db 6540 GTTGTATATAAATATATCA 6559

RESULT 3
US-09-233-527-1
Sequence 1, Application US/09233527
Patent No. 646617
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Hengartner, Michael
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
FILE REFERENCE: 01997/201004
CURRENT APPLICATION NUMBER: US/09/233,527
CURRENT FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: 07/898,933
PRIOR FILING DATE: 1992-06-12
PRIOR APPLICATION NUMBER: 07/927,681
PRIOR FILING DATE: 1992-08-10
PRIOR APPLICATION NUMBER: 08/288,295
PRIOR FILING DATE: 1994-08-10
PRIOR APPLICATION NUMBER: 08/801,248
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6559
TYPE: DNA
ORGANISM: Caenorhabditis elegans
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(6559)
OTHER INFORMATION: n = A,T,C or G
US-09-233-527-1

Query Match 99.5%; Score 6529.8; DB 4; Length 6559;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6559; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ATCGATAGTCGTACCAATGATTTTCGATTTCTCACTAGTCAGTCAGCTCACAATTTA 60
Db 1 ATCGATAGTCGTACCAATGATTTTCGATTTCTCACTAGTCAGTCAGCTCACAATTTA 60
Qy 61 CAAATATCGAAGAAAGAGATGCAAGAGATGAAGAGGTTCCGAAATCTAATATTT 120
Db 61 CAAATATCGAAGAAAGAGATGCAAGAGATGAAGAGGTTCCGAAATCTAATATTT 120
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US-09-234-186-2

Sequence 2, Application US/09234186

Patent No. 6312947

GENERAL INFORMATION:

APPLICANT: Horvitz, H. Robert

APPLICANT: Hengartner, Michael

TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A

TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND

FILE REFERENCE: 01997/201005

CURRENT APPLICATION NUMBER: US/09/234,186

EARLIER FILING DATE: 1999-01-20

EARLIER APPLICATION NUMBER: 07/899,933

EARLIER FILING DATE: 1992-06-12

EARLIER APPLICATION NUMBER: 07/927,681

EARLIER FILING DATE: 1992-08-10

EARLIER FILING DATE: 1992-08-10

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; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-234-186-2

Query Match          9.6%; Score 632.6; DB 4; Length 1315;
Best Local Similarity 99.8%; Pred. No. 5.9e-138;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1089 CCCTGAACCCCTAATTTTCTGCGCGCTAGACCTCCGCTGCTCCACATTTTCCA 1148
Oy 3873 AAGTACCCCTGATTCATTAATTCATCTTCACTTTAAGTGTCTGTTGCTGCTGCTG 3932
Db 1149 AAGTACCCCTGATTCATTAATTCATCTTCACTTTAAGTGTCTGTTGCTGCTGCTG 1208
Oy 3933 TTTCGACTCCCGCAAAATCTGTAAGCGGTAGCGGCACTTTGATTAATTTTCAATTT 3992
Db 1209 TTTCGACTCCCGCAAAATCTGTAAGCGGTAGCGGCACTTTGATTAATTTTCAATTT 1268
Oy 3993 GTTTTCCTCTCAACACACAAAAAAGCGTTC 4025
Db 1269 GTTTTCCTCTCAACACACAAAAAAGCGTTC 1301

```

RESULT 5

US-09-234-186-4

Sequence 4, Application US/09234186

Patent No. 6312947

GENERAL INFORMATION:

APPLICANT: Horvitz, H. Robert

APPLICANT: Hengartner, Michael

TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A

TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND

Db 969 TACGGCTCTCTGTGCGATTACGATTTTACTGCAATTTTTCOCATTCGCTTTT 1028
QY 3753 GGGCAAAACCTTACTTCCGGGTAATATCACTTTCCGTCTGTACATTTGCTCAAAA 3812
Db 1029 GGGCAAAACCTTACTTCCGGGTAATATCACTTTCCGTCTGTACATTTGCTCAAAA 1088
QY 3813 CCGTGAACCTTACTTCTTCCGCGGTACGCTCCCGCTCTCTCCATTTGCA 3872
Db 1089 CCGTGAACCTTACTTCTTCCGCGGTACGCTCCCGCTCTCTCCATTTGCA 1148
QY 3873 AAGTACCCCTGTATCTCAATATTTCACTTTACTGTCTCTTTCTGTGGCCTC 3932
Db 1149 AAGTACCCCTGTATCTCAATATTTCACTTTACTGTCTCTTTCTGTGGCCTC 1208
QY 3933 TTCCAACTCCCGCCAAATTCCTGTACGCGGACGCTTTGATTTATTTTTCAAAT 3992
Db 1209 TTCCAACTCCCGCCAAATTCCTGTACGCGGACGCTTTGATTTATTTTTCAAAT 1268
QY 3993 GTTTTCTCTCTACACACAAAAAAGGCTC 4025
Db 1269 GTTTTCTCTCTACACACAAAAAAGGCTC 1301

RESULT 9
US-09-233-527-4
; Sequence 4, Application US/09233527
; Patent No. 6465617
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 01997/201004
; CURRENT APPLICATION NUMBER: US/09/233,527
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-233-527-4

Query Match 9.6%; Score 632.6; DB 4; Length 1315;
Best Local Similarity 99.8%; Pred. No. 5.9e-138;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3393 GGACGACTTATGACACTCGGAAAAAATAAGAGGACTACGACAGAGAGAGCTGA 3452
Db 669 GGACGACTTATGACACTCGGAAAAAATAAGAGGACTACGACAGAGAGAGCTGA 728
QY 3453 AAAAGTGGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTGA 3512
Db 729 AAAAGTGGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTGA 788
QY 3513 TGGACCATTTGATCTGTGAGTGTCTGTGTGGCGGAGATGTTTCACTTGAAGTA 3572
Db 789 TGGACCATTTGATCTGTGAGTGTCTGTGTGGCGGAGATGTTTCACTTGAAGTA 848
QY 3573 ACGATTCATTTTGTGTAATTAATTATTTATGACACCTCTTACATTTGAATCTCAT 3632
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Db 849 ACGTATTCATTTTGTGTAATTAATTATTTATGACACCTCTTACATTTGAATCTCAT 908
QY 3633 TTGCTCATGATTTCTGCATCCCTTTGACGAGAGAGAGAGAGAGAGAGAGCTGA 3692
Db 909 TTGCTCATGATTTCTGCATCCCTTTGACGAGAGAGAGAGAGAGAGAGAGCTGA 968
QY 3693 TACGCTCTCTGTCTGATTTACGATTTTACTGCAATTTTTCGATTTGCTTTT 3752
Db 969 TACGCTCTCTGTCTGATTTACGATTTTACTGCAATTTTTCGATTTGCTTTT 1028
QY 3753 GGGCAAAACCTTACTTCCGGGTAATATCACTTTCCGTCTGTACATTTGCTCAAAA 3812
Db 1029 GGGCAAAACCTTACTTCCGGGTAATATCACTTTCCGTCTGTACATTTGCTCAAAA 1088
QY 3813 CCGTGAACCTTACTTCTTCCGCGGTACGCTCCCGCTCTCTCCATTTGCA 3872
Db 1089 CCGTGAACCTTACTTCTTCCGCGGTACGCTCCCGCTCTCTCCATTTGCA 1148
QY 3873 AAGTACCCCTGTATCTCAATATTTCACTTTACTGTCTCTTTCTGTGGCCTC 3932
Db 1149 AAGTACCCCTGTATCTCAATATTTCACTTTACTGTCTCTTTCTGTGGCCTC 1208
QY 3933 TTCCAACTCCCGCCAAATTCCTGTACGCGGACGCTTTGATTTATTTTTCAAAT 3992
Db 1209 TTCCAACTCCCGCCAAATTCCTGTACGCGGACGCTTTGATTTATTTTTCAAAT 1268
QY 3993 GTTTTCTCTCTACACACAAAAAAGGCTC 4025
Db 1269 GTTTTCTCTCTACACACAAAAAAGGCTC 1301

RESULT 10
US-09-233-527-5
; Sequence 5, Application US/09233527
; Patent No. 6465617
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 01997/201004
; CURRENT APPLICATION NUMBER: US/09/233,527
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-233-527-5

Query Match 9.6%; Score 632.6; DB 4; Length 1315;
Best Local Similarity 99.8%; Pred. No. 5.9e-138;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3393 GGACGACTTATGACACTCGGAAAAAATAAGAGGACTACGACAGAGAGAGCTGA 3452
Db 669 GGACGACTTATGACACTCGGAAAAAATAAGAGGACTACGACAGAGAGAGCTGA 728
QY 3453 AAAAGTGGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTGA 3512
|||||

Db 729 AAAAGTGGAGCCGGAAGACAGACAGCGTGTGATGATGAGCGCTGAGTAACAGC 788
Qy 3513 TGGAGCATTTGAAATCGTTGAGTGCCTGCTGCTGGCGGATGATGATGAGTGAAGTA 3572
Db 789 TGGAGCATTTGAAATCGTTGAGTGCCTGCTGCTGGCGGATGATGATGAGTGAAGTA 3572
Qy 3573 ACGTATTCATTTGTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3632
Db 849 ACGTATTCATTTGTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
Qy 3633 TTTGCTACATGATTTCTCATCTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3692
Db 909 TTTGCTACATGATTTCTCATCTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 968
Qy 3693 TACGCTCTCTGCTGCTGATTAAGATTTACTGCAATTTTTCGATTCGCTTTTTCCT 3752
Db 969 TACGCTCTCTGCTGCTGATTAAGATTTACTGCAATTTTTCGATTCGCTTTTTCCT 1028
Qy 3753 GGGCAAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3812
Db 1029 GGGCAAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1088
Qy 3813 CCCTGAACCCCTAATTTTCTGCGGCTGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCT 3872
Db 1089 CCCTGAACCCCTAATTTTCTGCGGCTGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCT 1148
Qy 3873 AAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1148
Db 1149 AAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1208
Qy 3933 TTCCAACTCCCGCCAAATTCCTGACGCTGACGCTGCTGCTGCTGCTGCTGCTGCTG 3992
Db 1209 TTCCAACTCCCGCCAAATTCCTGACGCTGACGCTGCTGCTGCTGCTGCTGCTGCTG 3992
Qy 3993 GTTTCTCTCTACACAACAACAAAAACGGTTC 4025
Db 1269 GTTTCTCTCTACACAACAACAAAAACGGTTC 1301

RESULT 11

US-09-233-527-6
; Sequence 6, Application US/09233527
; Patent No. 6465617
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201004
; CURRENT APPLICATION NUMBER: US/09233,527
; CURRENT FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-233-527-6

Query Match 9.6%; Score 632.6; DB 4; Length 1315;
Best Local Similarity 99.8%; Pred. No. 5.9e-138;

Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 3393 GGGAGCTTCTATACACTCGGAAACAAATGAAAGAGACTGACGAGAGAGAGAGAGAGAGAG 3452
Db 669 GGGAGCTTCTATACACTCGGAAACAAATGAAAGAGACTGACGAGAGAGAGAGAGAGAGAG 728
Qy 3453 AAAAGTGGAGCCGGAAGACAGACAGAGCGTGTGATGATGAGTGAAGTGAAGTGAAGTGAAGT 3512
Db 729 AAAAGTGGAGCCGGAAGACAGACAGAGCGTGTGATGATGAGTGAAGTGAAGTGAAGTGAAGT 788
Qy 3513 TGGAGCATTTGAAATCGTTGAGTGCCTGCTGCTGGCGGATGATGATGAGTGAAGTA 3572
Db 789 TGGAGCATTTGAAATCGTTGAGTGCCTGCTGCTGGCGGATGATGATGAGTGAAGTA 848
Qy 3573 ACGTATTCATTTGTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3632
Db 849 ACGTATTCATTTGTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
Qy 3633 TTTGCTACATGATTTCTCATCTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3692
Db 909 TTTGCTACATGATTTCTCATCTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 968
Qy 3693 TACGCTCTCTGCTGCTGATTAAGATTTACTGCAATTTTTCGATTCGCTTTTTCCT 3752
Db 969 TACGCTCTCTGCTGCTGATTAAGATTTACTGCAATTTTTCGATTCGCTTTTTCCT 1028
Qy 3753 GGGCAAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1028
Db 1029 GGGCAAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1088
Qy 3813 CCCTGAACCCCTAATTTTCTGCGGCTGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 3872
Db 1089 CCCTGAACCCCTAATTTTCTGCGGCTGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 1148
Qy 3873 AAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1148
Db 1149 AAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1208
Qy 3933 TTCCAACTCCCGCCAAATTCCTGACGCTGACGCTGCTGCTGCTGCTGCTGCTGCTG 3992
Db 1209 TTCCAACTCCCGCCAAATTCCTGACGCTGACGCTGCTGCTGCTGCTGCTGCTGCTG 3992
Qy 3993 GTTTCTCTCTACACAACAACAAAAACGGTTC 4025
Db 1269 GTTTCTCTCTACACAACAACAAAAACGGTTC 1301

RESULT 12

PCT-US93-05651-2
; Sequence 2, Application PC/TUS9305651
; GENERAL INFORMATION:
; TITLE OF INVENTION: A Gene Which Prevents Programmed Cell Death
; NUMBER OF SEQUENCES: 5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05651
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1315 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..846
; OTHER INFORMATION: /product= "Ced-9"
PCT-US93-05651-2

Query Match 9.6%; Score 632.6; DB 5; Length 1315;
Best Local Similarity 99.8%; Pred. No. 5.9e-138;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY	3393	GGAGACACTTATGACACTGCGAAACAAATGAAAGGAGACTACGAACGCGAGAGCTGA	3452
Db	669	GGAGACACTTATGACACTGCGAAACAAATGAAAGGAGACTACGAACGCGAGAGCTGA	728
OY	3453	AAAGTGGAGCGCGGAGAGCAAGACAGCGTGTCATGATTTGGCGCTGGAGTAAACG	3512
Db	729	AAAGTGGAGCGCGGAGAGCAAGACAGCGTGTCATGATTTGGCGCTGGAGTAAACG	788
OY	3513	TGGAGCACTTGGAAATCGTTGGAGTCGTCGTGTGGGGCGATGATTTGAGCTGAAGTA	3572
Db	789	TGGAGCACTTGGAAATCGTTGGAGTCGTCGTGTGGGGCGATGATTTGAGCTGAAGTA	848
OY	3573	ACGATTCATTTGTGTAATAATTAATTTATGTACAACTCCTTACATTTGAATCTCANT	3633
Db	849	ACGATTCATTTGTGTAATAATTAATTTATGTACAACTCCTTACATTTGAATCTCANT	908
OY	3633	TTTGCTCAGATTCCTCTCATCCCTTTGAACAGGAAGTGGGAAAGCTAAGCCACAAAT	3693
Db	909	TTTGCTCAGATTCCTCTCATCCCTTTGAACAGGAAGTGGGAAAGCTAAGCCACAAAT	968
OY	3693	TACGGCTCGTGTGCGATTTACGATTTTACTGCAATTTTTCGATTTGCGCTTTT	3753
Db	969	TACGGCTCGTGTGCGATTTACGATTTTACTGCAATTTTTCGATTTGCGCTTTT	1022
OY	3753	GGCCAAACCCTAAGTTCGGCGTAATATCAACTTTTCGCTGTGTGTACATTTGCGCAAAA	3813
Db	1029	GGCCAAACCCTAAGTTCGGCGTAATATCAACTTTTCGCTGTGTGTACATTTGCGCAAAA	1088
OY	3813	CCGTGAACCTTAACATTTTTCGCGCGGTAGCGCTTCGCTTCCTCCACATTTTCCA	3873
Db	1089	CCGTGAACCTTAACATTTTTCGCGCGGTAGCGCTTCGCTTCCTCCACATTTTCCA	1144
OY	3873	AAGTACCCCTGTATCTCAATATTTATCTTACCTTACGTCTCTTTCGTTGGGCGTC	3933
Db	1149	AAGTACCCCTGTATCTCAATATTTATCTTACCTTACGTCTCTTTCGTTGGGCGTC	1209
OY	3933	TTCGCACTCCCGCCAAATTCGTACGCGGTACGCGACTTTGTATTTATTTTTCAAAT	3993
Db	1209	TTCGCACTCCCGCCAAATTCGTACGCGGTACGCGACTTTGTATTTATTTTTCAAAT	1269
OY	3993	GTTTTCTCTACACACAAAAAAGCGTTC	4025
Db	1269	GTTTTCTCTACACACAAAAAAGCGTTC	1301
RESULT 13			
US-08-394-189B-1/C			
Sequence 1, Application US/08394189B			
Patent No. 5962301			
GENERAL INFORMATION:			
APPLICANT: Horvitz, Robert			
APPLICANT: Yuan, Junyang			
APPLICANT: Shahan, Shai			
TITLE OF INVENTION: RELATEDNESS OF HUMAN INTERLEUKIN-1			
TITLE OF INVENTION: BETA CONVERTASE GENE TO A C. ELBANS CELL DEATH			
TITLE OF INVENTION: GENE INHIBITORY PORTIONS OF THESE GENES AND...			
NUMBER OF SEQUENCES: 27			
CORRESPONDENCE ADDRESSES:			
ADDRESSEE: Clark & Elbing LLP			
STREET: 176 Federal Street			
CITY: Boston			
STATE: MA			
COUNTRY: USA			
ZIP: 02110			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Diskette			
COMPUTER: IBM Compatible			
OPERATING SYSTEM: DOS			
SOFTWARE: FastSeq for Windows Version 2.0			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/394,189B			
FILING DATE: 24-FEB-2005			

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? FILING DATE: 10-JUN-1994
? CLASSIFICATION: 435
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: US 08/080,850
? FILING DATE: 24-JUN-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Bugalsky, Lawrence B.
? REGISTRATION NUMBER: 35,086
? REFERENCE/DOCKET NUMBER: 0609.3920001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 371-2500
? TELEFAX: (202) 371-2540
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 7653 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: both
? TOPOLOGY: both
? FEATURE:
? NAME/KEY: CDS
? LOCATION: join(2232..2366, 2430..2576, 2855..3109, 4305
? LOCATION: ..4634, 5547..5759, 5817..5942, 6298..6537, 7012
? LOCATION: ..7075)
US-08-258-287B-1

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Query Match      2.1%; Score 139.2; DB 3; Length 7653;
Best Local Similarity 73.3%; Pred. No. 9.5e-23;
Matches 211; Conservative 0; Mismatches 63; Indels 14; Gaps 2;

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QY 3063 TGTATTGTTACGGAATACAAATTCGAGATGCTATTTCACACATATTGACGGC 3122
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DB 1635 TGAATATTATTCGGAACACAAATTCAGAGATGCTATTACAGTCATATTGGCGGC 1576
QY 3123 AAAATATCCAGTAGAGAAACTACAGTAATCTTTAAAT-----TTTAAATTTTAC 3176
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DB 1575 AAAATATCTCGTAGCTACAGTACAGTAATCTTTAAATGACTGCTAGCGTTGTACG 1516
QY 3177 AATTAAAGAAATTAACCACTAATCAAAAGAAATTAATTTCAAAAATCGAGCCGTAATC 3236
    || || || || || || || || || || || || || || || || || || || ||
DB 1515 AATTACGGGTATCAAAATTCGAAAAAATTAATTTCAAAAATGAGCCGTAATC 1456
QY 3237 GA-----CTACAGTAGGATTTAAAGATTTACTGAGTTTTCGCTACAGATATTTC 3288
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DB 1455 GACACAGCGCTACAGTAGTCAATTTAAAGAAATTTCTGAGTTTCGCTACAGATATTTC 1396
QY 3289 CGCCTCAAAATATGTTGTAATACGATTCACGATTTTGTGTTCC 3336
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DB 1395 GCCGCAAAATATGTTGCGCCAGTACGCAATTCACGAATTTTGTGATTC 1348

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RESULT 15
US-08-368-704C-1/c
? Sequence 1, Application US/08368704C
? Patent No. 6087160
? GENERAL INFORMATION:
? APPLICANT: Yuan, Junying
? APPLICANT: Miura, Masayuki
? TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
? NUMBER OF SEQUENCES: 95
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Sterne, Kessler, Goldstein & Fox
? STREET: 1100 New York Avenue, Suite 600
? CITY: Washington
? STATE: D.C.
? COUNTRY: USA
? ZIP: 20005
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:

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? APPLICATION NUMBER: US/08/368,704C
? FILING DATE: 4-JAN-1995
? CLASSIFICATION: 435
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: US 08/258,287
? FILING DATE: 10-JUN-1994
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/080,850
? FILING DATE: 24-JUN-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Bugalsky, Lawrence B.
? REGISTRATION NUMBER: 35,086
? REFERENCE/DOCKET NUMBER: 0609.3920002
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 371-2600
? TELEFAX: (202) 371-2540
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 7653 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: both
? TOPOLOGY: both
? FEATURE:
? NAME/KEY: CDS
? LOCATION: join(2232..2366, 2430..2576, 2855..3109, 4305
? LOCATION: ..4634, 5547..5759, 5817..5942, 6298..6537, 7012
? LOCATION: ..7075)
US-08-368-704C-1

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Query Match      2.1%; Score 139.2; DB 3; Length 7653;
Best Local Similarity 73.3%; Pred. No. 9.5e-23;
Matches 211; Conservative 0; Mismatches 63; Indels 14; Gaps 2;

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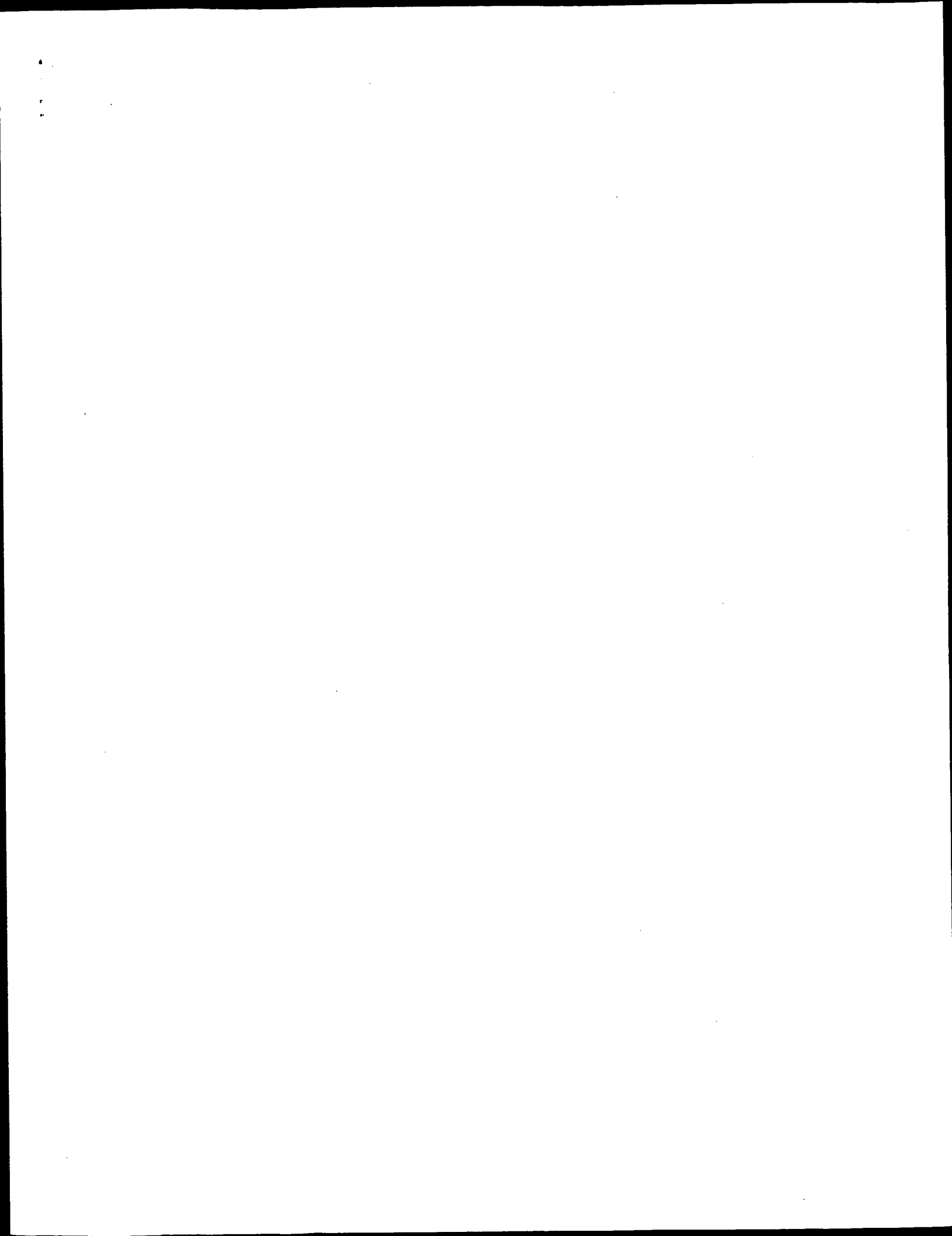
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DB 1575 AAAATATCTCGTAGCTACAGTACAGTAATCTTTAAATGACTGCTAGCGTTGTACG 1516
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    || || || || || || || || || || || || || || || || || || || ||
DB 1515 AATTACGGGTATCAAAATTCGAAAAAATTAATTTCAAAAATGAGCCGTAATC 1456
QY 3237 GA-----CTACAGTAGGATTTAAAGATTTACTGAGTTTTCGCTACAGATATTTC 3288
    || || || || || || || || || || || || || || || || || || || ||
DB 1455 GACACAGCGCTACAGTAGTCAATTTAAAGAAATTTACTGAGTTTCGCTACAGATATTTC 1396
QY 3289 CGCCTCAAAATATGTTGTAATACGATTCACGATTTTGTGTTCC 3336
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Search completed: February 28, 2003, 04:35:12
Job time : 366.757 secs

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Qy	3237	GA-----CTACAGAGGCATTTAAAGAAATTAAGTCTGAGTTTCGTCAGAGATATTC	3288
Db	1455	GACACAAAGCGTACAGTAGATCAATTTAAAGAAATTAAGTCTGAGTTTCGTCAGAGATATTTT	1356
Qy	3289	CGCCTCAAAATATGTTGGAATATACGCAATTCACAGATTTTGTGTTCC	3336
Db	1385	GCCTCAAAATATGTTGGCAGTAGACGATTCAGAAATTTGTGATATCC	1348

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RESULT 2
US-09-888-243-1
; Sequence 1, Application US/09888243
; Patent No. US20020136714A1
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Yuan, Junying
; APPLICANT: Shaham, Shai
; TITLE OF INVENTION: Relatedness of Human Interleukin-1beta
; TITLE OF INVENTION: Convertase Gene to a C. Elegans Cell Death Gene, Inhibitory
; TITLE OF INVENTION: Portions of these Genes and Uses Therefor
; FILE REFERENCE: 01997/211003
; CURRENT APPLICATION NUMBER: US/09/888, 243
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 09/083,662
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 08/394, 189
; PRIOR FILING DATE: 1995-02-24
; PRIOR APPLICATION NUMBER: US 08/282, 211
; PRIOR FILING DATE: 1994-07-11
; PRIOR APPLICATION NUMBER: US 07/984, 182
; PRIOR FILING DATE: 1992-11-20
; PRIOR APPLICATION NUMBER: US 07/897, 788
; PRIOR FILING DATE: 1992-06-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 7653
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-888-243-1

```

	Query Match	Similarity	1.6%	Score	No. 1.8:	DB 10;	Length	7653;
	Best Local	Similarity	69.5%;	Pred	No. 1.1e-10;			
Matches	207;	Conservative	0;	Mismatches	60;	Indels	31;	Gaps
Qy	5960	AATGCGCAACATATTGTGACCGCAAAATATCTGTAAGC-AAACATCATGAATTTCTTCAA						6018
Db	1374	ACTGGCCAAACAATTTTGACGGCAAAATATCTGTAGCGAAACATACAGTAATTTCTTTAA						1433
Qy	6019	AGACATCTAGTAGGC-TGTGTGATTTAGAGCTCATTTTGAATVGAATGAGACTAGA						6077
Db	1434	TGACTACTAGCGCTGTGTGTCATTTTAGGGGCTCAATTTTGAATAATTTTTTTTTT						1493
Qy	6078	AGAAAAGGAGAAATATTGACATCATTAATTGAACATCAATTCAAAAAGTCGAACCTTGA						6137
Db	1494	CGAATTTTGATTAACCGGTAAATCTGA-----CAACG						1525
Qy	6138	CTACACTAGTCTCTTAAABAATTTACTGTAGTTTCGCTACGAGATATTTTGNMGTCAAA						6197
Db	1526	CTACATATATCATTTAAAGATTACTGTAGTTCTACTCTAGAGATATTTTGGCCCCAANA						1585
Qy	6198	TATGTTNGCAATACCATCTTCAGAAATGTGTGTTCTCGTAATGTCTTGAANAATTT						6255
Db	1586	TATG-ACGTAAATGCCATTTCTGAAATTTTGTTTCGTAATTAATTTTACACAGAT						1642

```

US-09-945-258-11/c
? Sequence 11, Application US/09945258
? Patent No. US20020058276A1
? GENERAL INFORMATION:
? APPLICANT: St.George-Hyslop, Peter H.
? APPLICANT: Fraser, Paul E.
? TITLE OR INVENTION: PROTEINS RELATED TO SCHIZOPHRENIA AND USES THEREOF
? FILE REFERENCE: 1034/1H570
? CURRENT APPLICATION NUMBER: US/09/945,258
? CURRENT FILING DATE: 2001-08-31
? PRIOR APPLICATION NUMBER: US 60/229,889
? PRIOR FILING DATE: 2000-09-01
? NUMBER OF SEQ ID NOS: 19
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 11
? LENGTH: 4560
? TYPE: DNA
? ORGANISM: C. Elegans
US-09-945-258-11

```

Query Match	1.4%	Score 93;	DB 10;	Length 4560;
Best Local Similarity	72.4%	Pred. No. 5e-09;		
Matches 134;	Conservative	0;	Mismatches 50;	Indels 1; Gaps
Qy	4672	TCCTTACACGAAATTTTGGCATTTTGTGACCTTAATAATACGATACCTGGTCTCGACACGAA	47311	
Db	4304	TCCAGACCCGCGATTTTGGCATTTTGTGCTCCAAAATACGGTACCCGGTATCGACACGAT	42454	
Qy	4732	ACATTTTGGTAAATTCGAAAAAGATGCGCCCTTTAAAGATGCTGATGTTGAAC--TT	4790	
Db	4244	GAAATTTTGTGAATTCGAAAAAGGTGTGCCCCCTTTAAAGATACGTATTTCTTGACACT	4185	
Qy	4791	CTGTGTGTCGGACATTTTCATCGATTTTGTAGCCCTTTTATAAGAAAAATGATATT	4850	
Db	4184	CATTCTCTGCAATTTTTCATCGATTTTCTCAACTTTATGATTAATAAAATGCATTT	4125	
Qy	4851	ATTTA	4855	
Db	4124	TTTTA	4120	

```

US-09-945-258-11
RESULT 4
; Sequence 11, Application US/09945258
; Patent No. US20020058276A1
; GENERAL INFORMATION:
; APPLICANT: St. George-Hyslop, Peter H.
; APPLICANT: Fraser, Paul E.
; APPLICANT: University of Toronto
; TITLE OF INVENTION: PROTEINS RELATED TO SCHIZOPHRENIA AND USES THEREOF
; FILE REFERENCE: 1034/1H570
; CURRENT APPLICATION NUMBER: US/09/945,258
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,889
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 4560
; TYPE: DNA
; ORGANISM: C. Elegans
US-09-945-258-11

```

Query Match	Similarity	Score	Length
Best Local	58.9%	79.8	4560
Matches 155	Conservative	Pred. No. 2.1e-06	
		Mismatches 107	Indels 1
			Gaps 1

QY	4544	AAAAAGACCTAAAAAGCCCTAAAAATTTGAAGTTTCCACCTGTTTCCAAAGAAAGACCGA	4603
DB	3859	AAAAATTATTCACAAATAATATTCACACAGCTTTCGACGTTCTGCTTTGCAAAATATCAGAGAT	3918
QY	4604	ATTGCACAGCTTATTCACAGAGATTTCGATTAATTTGATTTGAAATTTTCAATTTTCATCTATCC	4663

D _b	3919	TTGCGATTAAAGAAACCTACATTT-IGATCAGTITTTCTTAATCTTTAGAGCAATTATAC	397777
Q _Y	4664	CCAAACGTCTTTACACGAAATTTTCGATTTTTCAGTTAAATACGATACCTGGTCC	47223
D _b	3978	TCGATTTGATGCCCGAGAAAAGTTTCGACTTTTGAGCCAAAAGCAGGTGCGAGGTCC	40373
Q _Y	4724	GACACGAAACATTTTGTTAATTCAAAAAGATGTGCGCTTTTAAAGAGTGTGAGTTT	47833
D _b	4038	GACACGAAAAATTATATTATTTGAAAATAATGTTCGCTTTTAAATGCTACTGATTTT	40973
Q _Y	4784	GAAACTCTGTGTGCGAGCTT	4806
D _b	4098	CGAATTCATTCGTGCGCAITTT	4120

```

RESULT 5
US-09-973-451-38
; Sequence 38, Application US/09973451
; Patent No. US2002013238A1
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AM, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE
; TITLE OF INVENTION: (PARG) ENZYMES,
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
; FILE REFERENCE: NTAD 201
; CURRENT APPLICATION NUMBER: US/09/973,451
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US/09/302,812
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/0083,768.
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 38
; LENGTH: 29793
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; US-09-973-451-38

```

Query Match	1.0%	Score 68.6	DB 10	Length 29793
Best Local Similarity	68.6%	Pred. No. 0.00076		
Matches 109	Conservative 0	Mismatches 49	Indels 1	Gaps 1
QY 4683	AAATTTGCATTTTTCGAGCTTAAATATAGATACCGGCTGTGACACGAAACATTTTGGT	4742		
Db 5611	ATTTTCATATCTCTGATGTGAAAAAATATACGGTACCCGATCTGGATACATACA-ATTTTTCGA	5669		
QY 4743	AAATTTAAAAAGATGTGGCGCCTTTAAAGAGTCTGTAGTTGAAACTTCTGTTGGCGG	4802		
Db 5670	AAATGCGAAAAAGTTTGCACCTTTAAAAAGAACATGCAATTTCAACACCTGTGGCTGG	5729		
QY 4803	ACCTTTCATCGATTTTTCGTACCGTTTTTTTATATAAGAA	4841		
Db 5730	ATTTGTTATCGGTTTTTAATATTTTTCGTAGAGTAA	5768		

```

RESULT 6
US-10-024-623-31
; Sequence 31, Application US/10024623
; Publication No.: US20020187524A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A. J.
; TITLE OF INVENTION: 8039, 46455, 54414, 53763, 67076, 67102, 44181,
; TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: MNT-214CP
; CURRENT APPLICATION NUMBER: US/10/024,623
; CURRENT FILING DATE: 2001-12-17

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; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ. ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 25002
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-10-024-623--31

```

Query Match	1.0%	Score 67.6	DB 9	Length 25002
Best Local Similarity	64.9%	Pred. No. 0.0011		
Matches 100	Conservative	0	Mismatches 54	Indels 0
			Gaps	0
QY 3238	ACTACAGTAGGCAATTAAAGAAATTA	CTAGTGTTCGCTACAGATAATTC	CGGCTCAAA	3297
DB 22788	AGTACAGAACTCATTAATAATTTGTT	TAAGTTCGCTACAGATATATTC	CGGGCTCAA	22847
QY 3238	TATGTGTGAAATACGCAATTCACGGA	TTTTGTGTCCCGGAATATGCTCTAA	AGCATT	3357
DB 22848	TATGTTCGCGAAATACGCAATTC	CAAAACGTACTGTCCGTAAATAT	ATGTTTCATTCT	22907
QY 3358	ATTGTGAAATATAAAAATCAAGAAAA	AAAAATTCG	3391	
DB 22908	GCTTCAAAACCTAATATTTTATATTA	TATACGTAAGC	22941	

```

RESULT 7
US-10-024-623-31/c
; Sequence 31, Application US/10024623
; Publication No. US20020187524A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 8099, 46455, 54414, 53763, 67076, 67102, 44181,
; TITLE OF INVENTION: 67064FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
; FILE REFERENCE: MNI-214CP
; CURRENT APPLICATION NUMBER: US/10/024,623
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 25002
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-10-024-623-31

```

Query Match	1.0%	Score 64.6	DB 9	Length 25002
Best Local Similarity	68.7%	Pred. No. 0.0044		
Matches 103	Conservative	0	Mismatches 42	Indels 5
			Gaps	1
QY 6129	AACCTTGATACAGTACGCTCTCTAAAGATATACGATGTTTCGTCACGAGAT-----A	6183		
Db 22393	AAACGATCTCTACGGTAGTCATCTATAAAGTTGCTGTGATTTTGGCTTCGTCACAAATCA	22334		
QY 6184	TTTTGNGTGCATATATGTTGNGCAATACGACATCCTCAGAAATTGTGTTCGTCTAATGT	6243		
Db 22333	TTTTGCGCGCAATATATGTTGTGCATATACGACCTTTTCAGTATTAGTGTTCCGTAATAT	22274		
QY 6244	CTTGAAATTTTCCATTTCAACATCAATA	6273		
Db 22273	TTATATTTTATTACTATTAGAAAAAAA	22244		

RESULT 8
US-09-973-451-38/c
; Sequence 38, Application US/09973451
; Patent No. US20020132328A1
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AM, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOPHROLASE
; TITLE OF INVENTION: (PARC) ENZYMS, AND ANTIBODIES IMMUNOREACTIV
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV
; FILE REFERENCE: NIND 201
; CURRENT APPLICATION NUMBER: US/09/973,451
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US/09/302,812
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/083,768
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 38
; LENGTH: 29793
; TYPE: DNA
; ORGANISM: *Caenorhabditis elegans*
; FEATURE:
US-09-973-451-38
Query Match 1.0%; Score 63.4; DB 10; Length 29793;
Best Local Similarity 72.6%; Pred. No. 0.0082;
Matches 82; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 4676 TACAGCAATTTTCGATTTTTCGATTTTAAATACGATACCTGCTGCACAGCAAAAT 4735
DB 5914 TATGTGAATTTTCGACATTTTAAATGCAAAATCAGCGTACCGGTTTCGACAGCAAAAT 5855
QY 4736 TTTTGTAAATTTCAAAAAGATGCGCCTTTAAAGAGCTGTGATTTGAAC 4788
DB 5854 GTTGTATATAGCAAAATGCGTGTCTTTGAAAAGTACTGATTTCAATC 5802
RESULT 9
US-09-938-842A-4849
; Sequence 4849, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kieps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4849
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: *Arabidopsis thaliana*
US-09-938-842A-4849
Query Match 0.9%; Score 56; DB 9; Length 2000;
Best Local Similarity 51.3%; Pred. No. 0.084;
Matches 155; Conservative 0; Mismatches 145; Indels 2; Gaps 1;

QY 2366 TCTTTTGGAAAGTTTTCATTAAAAACCAAGATTTTGATCCGGATGTGTAATTTT 2425
DB 1517 TTTAATTTTACAAATTTTCAAAATATACCGAATTTTAAATCGATTAATTAATTT 1576
QY 2426 TTGTGATTAATTTACGAGAACTTTACGAATTCATTAATAAAGCTTTTTCATTCGA 2485
DB 1577 AATTTTCAAAAAAACAACGATTTAAATAATTAATTAATTAATTAATTAATTAATTA 1636
QY 2486 ATATTTTAAACGATTTTCCGTGATTTGATTTGCGAAAAAGATTCGATTAATTA 2545
DB 1637 ATTTTGTATTAATTAATTTT--TTTATACCTTAACGATTAATTAATTAATTAATTA 1694
QY 2546 AAAATCGTTTTTAAATGTAATTTTGGAATAATACATTAATTCGATTTTGAAGCTT 2605
DB 1695 TAAAGTTTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1754
QY 2606 TTTTCTGAAAAACAGTTTTTTCGATTTGCTGTAACGAAAAACCCCAATTAATTA 2665
DB 1755 AACTTTTGAACAAATTTTTCGTAATAATTAATTAATTAATTAATTAATTAATTAATTA 1814
QY 2666 TT 2667
DB 1815 TT 1816
RESULT 10
US-09-960-352-4584/c
; Sequence 4584, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Ningbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4584
; LENGTH: 416
; TYPE: DNA
; ORGANISM: *Bos taurus*
; OTHER INFORMATION: Clone ID: 20-LIB3057-016-Q1-K1-E11
US-09-960-352-4584
Query Match 0.8%; Score 53; DB 10; Length 416;
Best Local Similarity 46.0%; Pred. No. 0.18; Indels 210; Gaps 0;
Matches 179; Conservative 0; Mismatches 210; Indels 0; Gaps 0;
QY 2303 AAAAATGTTTGTTCCTTCAGAAATCAGCAAACTTGCAAAAATAGCCCAATTA 2362
DB 412 AAAATTTTGTTCCTTCAGAAATCAGCAAACTTGCAAAAATAGCCCAATTA 353
QY 2363 GTGTCTTTTGAAGTTTTCATTAATAAACACGAAATTTGATCCGGAATGTAATTT 2422
DB 352 CATATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 293
QY 2423 TTTTGTGATTAATTTACGAGAACTTTACGAATTCATTAATAAAGCTTTTTCATTT 2482
DB 292 AATTTTAAATTTTAAATAATTTTCTTTAAATAATTAATAATTTTAAATAATTTT 233
QY 2483 CGAATATTTTAAACGATTTTCCGTGATTTGATTTGCGAAAAAGATTCGATTAATTA 2542
DB 232 TTTTGTGATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 173
QY 2543 TCAAAAATCGGTTTTTAAATGTAATAATTTTGGAATAATTAATTAATTAATTAATTT 2602
DB 172 TTTTGTGATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 113
QY 2603 CTTTTCCTGCAAAAACGTTTTTTCGTCGATTTGCTGAACGAAAAACCCCAATTA 2662

PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676

PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 0.8%; Score 51.6; DB 9; Length 2773;
Best Local Similarity 55.6%; Pred. No. 0.72; Indels 0; Gaps 0;
Matches 99; Conservative 0; Mismatches 79;

QY 428 AAGGTCATTTTGAAGCCGAAATTTTACTAAATCTCTAGCCATGAGTGCATGCAG 487
DB 2592 AAATTCATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2651
QY 488 AAATTCGAGAAATTTAGATTTTCATCTTGAATTTTCAATGCAAAATTAATTTCAA 547
DB 2652 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2711
QY 548 GAAATTCACGAAATTCGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 605
DB 2712 AA 2769

RESULT 13
US-09-989-293A-178
Sequence 178, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.

APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumus, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730pic66
 CURRENT APPLICATION NUMBER: US/09/989,293A
 PRIOR FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
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Thu Mar 6 08:14:02 2003

us-09-993-420a-1.rnpb

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Query Match	0.88;	Score 51.6;	DB 9;	Length 2773;
Best Local Similarity	55.6%;	Pred. No. 0.72;		
Matches 99;	Conservative	0;	Mismatches 79;	Indels 0;
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Search completed: February 28, 2003, 10:05:45
Job time : 1163.42 secs


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Oy 2667 TTTGCAATTAATAAACGAAAAATCGTTTTTAAGCTTAATTTCCGCAAGAAATGA 2726
Db 600 WBBBGAHAHYMMBYBAKCHCMKAMYKAKYAGAGSGNNNNNNNNNNNNNNNNATCAR 659
Oy 2727 ACGAATTAATTCGAATTTCTAATTTTCAGATAGCTTAATCTGCTGGCGTTTGT 2786
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Db 780 YTTNNNNNTYRGVYNTAAADGWAANNNNNNNNNNNNNNNNNGSDWVYTWVYANTGNNNN 839
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Oy 3027 TCGAACAATATCAAGTATTTACTGTTTATGTAATGTTATGTTACGGGATACAAA 3086
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Oy 3087 TTGCAAGATGCTATTTTACACATATTTGACGCGCAAAATATCCAGTAGAGAAATAC 3146
Db 1019 YWIGWKTWTAIRATIRATIRATIRATIRATIRATIRATIRATIRATIRATIRAT 1078
Oy 3147 AGTAATTTCTTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3204
Db 1079 GKATCYMDNAAWMTACATSMWATHKYMHMCCKNNNNNNNNNNNNNNNNNNNNNN 1136

RESULT 2
US-09-806-708B-22/c
: Sequence 22, Application US/09806708B
: GENERAL INFORMATION:
: APPLICANT: The University of British Columbia
: TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
: FILE REFERENCE: 4810-58741
: CURRENT APPLICATION NUMBER: US/09/806,708B
: PRIOR FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 22
: LENGTH: 1141
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: NAME/KEY: Promoter
: LOCATION: (1)..(1141)
: OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

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Query Match 1.0%; Score 66; DB 5; Length 1141;
Best Local Similarity 13.2%; Pred. No. 0.0018;
Matches 122; Conservative 332; Mismatches 461; Indels 12; Gaps 3;

Oy 2216 ATGCACGTTTGTGAAGGAGAAAAATCTGAAAAAAAGTTTGCAGAAAATTCGCG 2275
Db 1003 ATNNAMVATTTBMAAAYAAAKWABAGNNMREYGAAGNKKCAAAATBMBWADTAGK 944
Oy 2276 CAGAAAGTGGCAGAAAAAATTTGCA---AAATGTTGTTTCTCCCTCAGAAATC 2331
Db 943 CNNNNNNMTDVRMAKAKNNNNNNNAVYACINRAATNNKATTHMKYTHGASHRRR 884
Oy 2332 AGCAAAATTCGTCAAAAATAGCCCAATATGTCCTTTTGAAGTTTCCATTAAAA 2391
Db 883 HHHTCCRTKYNNNNNNARVYVYHHAARRMNAWMTRTNNNNNNNNNNNNNNNNNN 824
Oy 2392 AACAAGATTTGATCCCGGATTTGTAATTTTGTGATAATATAGAGAAATCTT 2451
Db 823 WKHSVCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 764
Oy 2452 ACGAATCGATTAATAACGTTATTTCTAATTCGAATATTTTAAAGCATATTTCTTGA 2511
Db 763 HTDWCTKWTWTTWDMATTTBTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTT 704
Oy 2512 TTTGATTTGCAAAAAGATCTGCTGATTTATCAAAAATCGTTTTTAATGTAAATTT 2571
Db 703 HATNNWGCWNNNTDARNTNTTVMRRMNTKTRWYSTRHHYTATNNNNNNNNNN 644
Oy 2572 GTGA-----AAATACATTAATTCGATTTTGAACCTTTTCTCGAAAAACAGTT 2625
Db 643 NNNNNSCCTGRMTTMTKMDGENTYKVKYKMDTCTTYDVADSDWVYAWMMCRD 584
Oy 2626 TTTCTGATTTGCTGCAAGCAAAAACCCCAAAATTCATTTTGAACATTTAAACCA 2685
Db 583 YTTTNNNTYCKSAISYVYNNNNMMWRYSARBNSSARRTTNNNNMWSGBVBRWAGT 524
Oy 2686 GAAAAATGTTTTTTTAAGCTTAATTTTCCCGCAGAAATGACGATTAATTCGAAT 2745
Db 523 MWRHNNNNNTDRTYVWMMKRBARTTYVDSMCAKSMRGNMNNRAKMMWAAANNDDGA 464
Oy 2746 TCTAATTTTCAATAGTCTATCTGCTGCGGCTTCTGAGTCCAAAAATGATGGA 2805
Db 463 MDHWITWMMNNNTMMRRKMMNNMMCRATCCNNNNNNNNNNNNNNNNNNNNNN 404
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Oy 2866 ACGCGATCCGCAACACGGAAGGACACATCGGAGCTGGTGAAGAGTATTCAT 2925
Db 343 KTTSMWMMNDHNTTCTGNNNTGSAUYBMAAASMAAGASNBVTYNKCRMTYMKTYTN 284
Oy 2926 GACATTGAAGTCAATATCCCTTCCCTAGTACCTTGAACCTCCGCGGCTGTTGTA 2985
Db 283 NNNNNKMYRTKRYTAVCMNNRRYVYDPAWTVBRNKYCAAYBYWYBMVKGHHMBMRA 224
Oy 2986 GCGGATTAATTAAGGTTGTAAGCTCTTGGGGGACAGCTGGAACATATTCAGAT 3045
Db 223 BHSNNMMWVVCNKRYVSMHYHAMRYBKWABAVG--CNNNNKDKBHHNNWATNNNNMM 166
Oy 3046 ATTACGTTTATGATATGTTATTTGTTAGGGGAATAACAATTCGAGAAATCTTTC 3105
Db 165 WMYAYMHHHKKKGAWTKNKTABRDBAHYKTYWYKTYDYWCAMCMWNAKAKRYTAMK 106
Oy 3106 CAACATATTTGACGCGCAAAATATCCA 3132
Db 105 HMYTDTDRYSANNITGVRRMMRMWCMW 79

RESULT 3
US-10-311-455-1955
: Sequence 1955, Application US/10311455

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Db 1039 AAAAAATTAATACTATTTTACCATATTTTAAATATAACAGC--TTAATTTCA 983
QY 2412 GATTTGAAATTTTGTGATTAATTTAGCAGAAATTTAGCATTTAAACAGT 2471
Db 982 TTTTTCCTAATTCACATTAATATTTATCATTTAAATTTAAATAAATCTTCTT 923
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Db 862 CAACATTTTAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 808
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QY 2652 CCCCCAAATTCATTTTGCACATTAATAACCAAGAAATCGTTTTTAAAGCTTAAT 2711
Db 747 CATTAAAT--AATTTTAAATAATTAATTAATTAATTAATTAATTAATTAATTA 691
QY 2712 TTCCGCGAATGAATGAATTAATTTGCAATTTCTAATTTTCAATAGTCTAA 2767
Db 690 TTATTTCTATTAATTAATTAATTTAAACCATTAATTAATTAATTAATTAATTA 635

RESULT 6
US-10-311-455-426
Sequence 426, Application US/10311455

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311.455
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 426
LENGTH: 6980
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-426

Query Match 0.8%, Score 55.6; DB 6; Length 6980;
Best Local Similarity 49.0%; Pred. No. 0.23;
Matches 148; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 2401 TTTTATCCCGATGTAATTTTGTGATTAATTAATTAATTAATTAATTAATTAAT 2460
Db 3415 TTTTATGAGTAGAGAAATTTTATGTTGATTAATTTTAAATTAATTAATTTTAA 3474
QY 2461 ATTTAAAGCTATTTTCATTCGAATATTTTAAAGCAATTTTCTGATTTGATTTT 2520
Db 3475 TTAATTAATTTTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3534
QY 2521 CGAAAAAGATGCTGATTTTCAAAAATCGTTTTTAATTAATTAATTTTGTGAAAT 2580
Db 3535 TTTATATGATAGTAAAGCTATTAAGAAATAGATTAAGATTAATTAATTAATTA 3594
QY 2581 ACATTAATTCGATTTTGAATTTTCTGAAATAACAGTTTTTCTGCTGATTTGC 2640
Db 3595 GTTTTGAATTTTGTGTTTTTTTGTGTTTTTTTAAATTAATTAATTAATTAATTA 3654

QY 2641 TGAACGAATAACCCCAAAATTCATTTTGCACATTTAAACAGAAATCGTTTTT 2700
Db 3655 TAAAGATTAATAATTTAAAGGATTTTATTTTATGATTAACAAAAAATGTTATTT 3714
QY 2701 TA 2702
Db 3715 TA 3716

RESULT 7
US-10-312-841-2
Sequence 2, Application US/10312841

GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des menschlichen Genoms
FILE REFERENCE: E01/1208/2WO
CURRENT APPLICATION NUMBER: US/10/312.841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 3673778
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
NAME/KEY: unsure
LOCATION: (379615)
US-10-312-841-2

Query Match 0.8%, Score 55.6; DB 6; Length 3673778;
Best Local Similarity 47.9%; Pred. No. 0.56; Indels 0; Gaps 0;
Matches 160; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

QY 2413 ATTTGATTTTGTGATTAATTTAGCAGAAATTTAGCAATTTGATTAATTAATTAAT 2472
Db 929075 ATTTTGTATATATTTATGATTAATTAATTAATTAATTAATTAATTAATTAAT 929134
QY 2473 ATTTTCTATTCGAATATTTTAAAGCAATTTTCTGATTTGATTTGATTTGATTTG 2532
Db 929135 TTTTATATTTAGATTAATTAAGAAAGTAAATGTTGATTAATTAATTAATTAATTA 929194
QY 2533 TGTGATTTATCAAAAATCGTTTTTAAATTTGATTAATTTGATTAATTTGATTTG 2592
Db 929195 TAGGTTTAAAGTAAATTTGATTAATTTGATTAATTTGATTAATTTGATTTGATTT 929254
QY 2593 GATTTTGAATTTTCTGCAAAAACAGTTTTTCTGATTTGCTGAACGAAATTC 2652
Db 929255 AATGTTAGTAGAGAGGAGGAAATTTAAGATTTGATTTAATTAATTAATTAATTA 929314
QY 2653 CCCCCAAATTCATTTTGCACATTTAAACCAAGAAATCGTTTTTAAAGCTTAATTT 2712
Db 929315 TATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 929374
QY 2713 TCCGCGAATGAATGAATTAATTTGCAAAATTT 2746
Db 929375 GTCTGATTAATTAATTAATTAATTTTAAATTT 929408

RESULT 8
US-10-311-455-1102
Sequence 1102, Application US/10311455

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311.455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537

Query Match	0.88;	Score 54.2;	DB 6;	Length 9157;
Best Local Similarity	45.1%;	Pred. No. 0.45;		
Matches 290; Conservative	0;	Mismatches 347;	Indels 6;	Gaps 3

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RESULT 10
US-10-311-455-1721
; Sequence 1721, Application US/10311455
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detection of Cytosine Methylation
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1721
; LENGTH: 11805
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1721

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Query Match	Similarity	0.88;	Score 54;	DB 6;	Length 1713;
Best Local	Similarity	46.4%;	Pred. No. 0.54;		
Matches	246;	Conservative	0;	Mismatches 280;	Indels 4; Gaps 2;
Qy	2243	TGAAAAAAGTTGCAAAAATTGGAATTCGCCAGAAAAGTGCAGAAAAACATTTGC	2302		
Db	9307	TAAAAAATATATACCTGCAAAAACATTTATATATACCAACAAATCAAAAATCATTTAA	9248		
Qy	2303	AAAAATGTTGTTTCCTTCAGGAATATAGCAAACTGTGCATAAATAGCCCAATTAT	2362		
Db	9247	ATAATATATATATAAAACACAAACTATAAAAAACAAATATATATAAAAAATCTAATAT	9188		
Qy	2363	GTCGTTTTTTGGAAGTTTTCCATTAAAAACCGAATTTTGATCCCGGATTTGTAATTT	2422		
Db	9187	TACTAAATCTACAAAAAATATATATATAAAAAATATAAAAAATCAACGAATTTTAAATA	9128		
Qy	2423	TTTTTGA-TGATAAATTAGCAGAAACTTTAGCAATTGCATTAATAAAGCTATTTTCTAT	2481		

[illegible]

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 18:42:50 : Search time 7944.47 Seconds
(without alignments)
13373.121 Million cell updates/sec

Title: US-09-993-420a-1

Perfect score: 6560
Sequence: 1 atcgatagtcgtcaccaaat.....gtttgtataaaattatcaaa 6560

Scoring table:

IDENTITY: NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estlin: *
4: em_estm: *
5: em_estov: *
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7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
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16: em_estrom: *
17: gb_gss: *
18: em_gss_hum: *
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21: em_gss_vrt: *
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23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rtd: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	554	8.4	672	9	AU214778 AU214778
C 2	544	8.3	640	9	AU216828 AU216828
C 3	533.4	8.1	706	13	BJ135657 BJ135657
C 4	529	8.1	593	13	BJ124068 BJ124068
C 5	514.8	7.8	638	13	BJ143512 BJ143512
C 6	513	7.8	587	13	BJ152426 BJ152426

C 7	473.4	7.2	556	9	AU215190 AU215190
C 8	470.8	7.2	562	13	BJ134935 BJ134935
C 9	433.4	6.6	606	13	BJ107235 BJ107235
C 10	365.4	5.6	515	9	AU203561 AU203561
C 11	324.6	4.9	502	13	BJ103911 BJ103911
C 12	323	4.9	501	9	AU202666 AU202666
C 13	323	4.9	502	13	BJ114579 BJ114579
C 14	322.4	4.9	500	13	BJ101104 BJ101104
C 15	318	4.8	360	9	AV190122 AV190122
C 16	314.6	4.8	323	14	D73048 D73048
C 17	312.4	4.8	372	9	AV186746 AV186746
C 18	311.4	4.7	676	13	BJ149838 BJ149838
C 19	308	4.7	377	14	CA47713 CA47713
C 20	307.2	4.7	488	9	AU214274 AU214274
C 21	304	4.6	377	9	AV191091 AV191091
C 22	303.4	4.6	709	13	BJ143970 BJ143970
C 23	303	4.6	377	14	CA49742 CA49742
C 24	302	4.6	360	14	C39347 C39347
C 25	301	4.6	376	9	AV192163 AV192163
C 26	300	4.6	375	9	AV195166 AV195166
C 27	299	4.6	300	9	AV181369 AV181369
C 28	297	4.5	375	14	CA2506 CA2506
C 29	295.8	4.5	360	9	AV192562 AV192562
C 30	285.4	4.4	360	9	AV201872 AV201872
C 31	279.6	4.3	300	14	C39078 C39078
C 32	275.6	4.2	300	14	C31912 C31912
C 33	274	4.2	482	13	BJ131523 BJ131523
C 34	273.2	4.2	307	14	M79968 M79968
C 35	269.8	4.1	300	9	AU113305 AU113305
C 36	269.2	4.1	300	14	C29364 C29364
C 37	268.2	4.1	300	9	AU112965 AU112965
C 38	267.2	4.1	300	9	AV199224 AV199224
C 39	265	4.0	300	14	AV114559 AV114559
C 40	259.4	4.0	300	9	AV179317 AV179317
C 41	256	3.9	300	9	AU114409 AU114409
C 42	256	3.9	300	9	AU114279 AU114279
C 43	254.6	3.8	510	3	AU218099 AU218099
C 44	250.4	3.8	510	3	AU218099 AU218099
C 45	247.8	3.8	300	9	AU116690 AU116690

ALIGNMENTS

RESULT 1
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LOCUS AU214778
DEFINITION AU214778 unpublished oligo-capped cDNA library, stage 12
ACCESSION AU214778
VERSION AU214778.1 GI:14852935
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE 1 (bases 1 to 672)
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2001)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"

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/clone_lib="unpublished oligo-capped cDNA library, stage
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/dev_stage="L2"
/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pCR86"
BASE COUNT      212 a      128 c      183 g      147 t      2 others
ORIGIN
Query Match      8.4%; Score 554; DB 9; Length 672;
Best Local Similarity 91.2%; Pred. No. 3.7e-78;
Matches 620; Conservative 0; Mismatches 7; Indels 53; Gaps 1;

QY 968 AGTCGAGCAAGAACGCAATCCAGAAATTCGATGGGATACCTGTGAGAGGCGT 1027
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DB 630 AGTCGAGCAAGAACGCAATCCAGAAATTCGATGGGATACCTGTGAGAGGCGT 571
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QY 1028 CCAAAATCGCCCAATGCTCCACATCTCAGCTACACCCACAAATTCGATGTC 1087
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DB 570 CCAAAATCGCCCAATGCTCCACATCTCAGCTACACCCACAAATTCGATGTC 511
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QY 1088 TCTCCGATTCATAGAAATCAGCGGTGTGTATGCGCGGAAACCTTCTCGGAGAA 1147
    |||||||
DB 510 TCTCCGATTCATAGAAATCAGCGGTGTGTATGCGCGGAAACCTTCTCGGAGAA 451
    |||||||
QY 1148 TCGGATTCGCAATTTTCCGCTTCGATTTTCACGCTTTTGTGATTCATCGTACCTGGA 1207
    |||||||
DB 450 TCGGATTCGCAATTTTCCGCTTCGATTTTCACGCTTTTGTGATTCATCGTACCTGGA 391
    |||||||
QY 1208 ACTTACATCGCGGTGACCGCTGTCTTCAATACATCATTCCTTCCCATCATTTTC 1267
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DB 390 ACTTACATCGCGGTGACCGCTGTCTTCAATACATCATTCCTTCCCATCATTTTC 331
    |||||||
QY 1268 ATACTCTTAACGGAATTCCTTCTTATGATTCGATTTGGCTAAGGAGTCAATATGTTG 1327
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DB 330 ATACTCTTAACGGAATTCCTTCTTATGATTCGATTTGGCTAAGGAGTCAATATGTTG 271
    |||||||
QY 1328 GACAGTAGAGATTGAATTAATTAATTTTAAATTAATTAATTTTTCAGAT 1387
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DB 270 GA-----CAGAT 264
    |||||||
QY 1388 CTACAAATCGGATATCTGATCTGATCTGCTATTTCTGCTCGCAATTCCTT 1447
    |||||||
DB 263 CTACAAATCGGATATCTGATCTGATCTGCTATTTCTGCTCGCAATTCCTT 204
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QY 1448 CAACCTCTTGCAAGAACGCAAGAACGATGCTGAGGACAGATGCTCGCTTCTT 1507
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DB 203 CAACCTCTTGCAAGAACGCAAGAACGATGCTGAGGACAGATGCTCGCTTCTT 144
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QY 1508 TTCTTACTCGCCGCCACCTCGCAATTCGTAATTTACTTTACGTTGATTTCTT 1567
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DB 143 TTCTTACTCGCCGCCACCTCGCAATTCGTAATTTACTTTACGTTGATTTCTT 84
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QY 1568 CGATTTTCTCTTTTCCGTAATTTACCTCTCTTCCGTTTCTTCTCTCTAGA 1627
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DB 83 CGATTTTCTCTTTTCCGTAATTTACCTCTCTCTTCCGTTTCTTCTCTCTAGA 24
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QY 1628 ATGTATATTATGATTATGAA 1647
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DB 23 ATGTATATTATGATTATGAA 4
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RESULT 2
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 LOCUS AU216828
 DEFINITION Ctenophoraditidis elegans cDNA clone yk842e12 3', mRNA sequence.
 ACCESSION AU216828

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VERSION AU216828.1 GI:14854985
KEYWORDS EST.
SOURCE Ctenophoraditidis elegans.
ORGANISM Ctenophoraditidis elegans
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae
AUTHORS ; Rhabditidae; Pelodierinae; Ctenophoraditidis.
1 (bases 1 to 640)
Kohara, Y., Shinn, I. T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
and Sugano, S.
A complementary view of the C. elegans genome
Unpublished (2001)
JOURNAL Genome Biology Lab.
CONTACT: Yui Kohara
NATIONAL INSTITUTE OF GENETICS
Yata 111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
FEATURES
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Location/Qualifiers
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/strain="N2"
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/clone_lib="unpublished oligo-capped cDNA library, stage
L4"
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/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pCR86"

```

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BASE COUNT      204 a      123 c      174 g      138 t      1 others
ORIGIN
Query Match      8.3%; Score 544; DB 9; Length 640;
Best Local Similarity 91.8%; Pred. No. 1.4e-76;
Matches 607; Conservative 0; Mismatches 1; Indels 53; Gaps 1;

QY 968 AGTCGAGCAAGAACGCAATCCAGAAATTCGATGGGATACCTGTGAGAGGCGT 1027
    |||||||
DB 618 AGTCGAGCAAGAACGCAATCCAGAAATTCGATGGGATACCTGTGAGAGGCGT 559
    |||||||
QY 1028 CCAAAATCGCCCAATGCTCCACATCTCAGCTACACCCACAAATTCGATGTC 1087
    |||||||
DB 558 CCAAAATCGCCCAATGCTCCACATCTCAGCTACACCCACAAATTCGATGTC 499
    |||||||
QY 1088 TCTCCGATTCATAGAAATCAGCGGTGTGTATGCGCGGAAACCTTCTCGGAGAA 1147
    |||||||
DB 498 TCTCCGATTCATAGAAATCAGCGGTGTGTATGCGCGGAAACCTTCTCGGAGAA 439
    |||||||
QY 1148 TCGGATTCGCAATTTTCCGCTTCGATTTTCACGCTTTTGTGATTCATCGTACCTGGA 1207
    |||||||
DB 438 TCGGATTCGCAATTTTCCGCTTCGATTTTCACGCTTTTGTGATTCATCGTACCTGGA 379
    |||||||
QY 1208 ACTTACATCGCGGTGACCGCTGTCTTCAATACATCATTCCTTCCCATCATTTTC 1267
    |||||||
DB 378 ACTTACATCGCGGTGACCGCTGTCTTCAATACATCATTCCTTCCCATCATTTTC 319
    |||||||
QY 1268 ATACTCTTAACGGAATTCCTTCTTATGATTCGATTTGGCTAAGGAGTCAATATGTTG 1327
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DB 318 ATACTCTTAACGGAATTCCTTCTTATGATTCGATTTGGCTAAGGAGTCAATATGTTG 259
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QY 1328 GACAGTAGAGATTGAATTAATTAATTTTAAATTAATTAATTTTTCAGAT 1387
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DB 258 GA-----CAGAT 252
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QY 1388 CTACAAATCGGATATCTGATCTGATCTGCTATTTCTGCTCGCAATTCCTT 1447
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DB 251 CTACAAATCGGATATCTGATCTGATCTGCTATTTCTGCTCGCAATTCCTT 192
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all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pCR8⁺

BASE COUNT 123 a 160 c 111 g 198 t 1 others

Query Match 8.1%; Score 529; DB 13; Length 593;

Best Local Similarity 91.6%; Pred. No. 3, 5e-74; Mismatches 592; Conservative 0; Mismatches 1; Indels 53; Gaps 1;

999 CGGATGGGAATACCTGTTGAGACAGCGCTCCAGAAATCGCCCAATGCTCCACATCTCAC 1058
 1 CGGATGGGAATACCTGTTGAGACAGCGCTCCAGAAATCGCCCAATGCTCCACATCTCAC 60
 1059 CGGTACACGCCACAAATGACCTGATGCTCCGATTCATGAAATCAGCGTTGTGT 1118
 61 CGGTACACGCCACAAATGACCTGATGCTCCGATTCATGAAATCAGCGTTGTGT 120
 1119 AATGGCCGGAACCTTCCTGCGAGAGAAATGCAATGCGCATTTGGCCGTTCATTCAC 1178
 121 AATGGCCGGAACCTTCCTGCGAGAGAAATGCAATGCGCATTTGGCCGTTCATTCAC 180
 1179 CGCTTTTGGATTCATCCGATGCTGACATTCACATGCGCGGTGACCGCTGCTTCAA 1238
 181 CGCTTTTGGATTCATCCGATGCTGACATTCACATGCGCGGTGACCGCTGCTTCAA 240
 1239 GTACATCATGCTTTCCCATCATCTTCTTACGGAATTCGCTTTAGAGATT 1298
 241 GTACATCATGCTTTCCCATCATCTTCTTACGGAATTCGCTTTAGAGATT 300
 1299 CGATTTGGCTAAGGAGATCAATATGTTGACAGTAGAGATTGAATTAATTAAT 1358
 301 CGATTTGGCTAAGGAGATCAATATGTTGACAGTAGAGATTGAATTAATTAAT 331
 1359 TGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1418
 332 -----CAGATCTCAAAATCGGGAATCTGATCTGAGACT 367
 1419 TCGGCTAATTCCTGCTCGCATTTGCTTCAACTCTTCCCAAGCAAGAGCAAAAGACT 1478
 368 TCGGCTAATTCCTGCTCGCATTTGCTTCAACTCTTCCCAAGCAAGAGCAAAAGACT 427
 1479 GCTTAGCAGCAAGATGCTCGGCTCTTTTCTTACTCGGCCCAAGCCCTCGCAATTC 1538
 428 GCTTAGCAGCAGATGCTCGGCTCTTTTCTTACTCGGCCCAAGCCCTCGCAATTC 487
 1539 CGTCAATTTACTTTTACCGTTGATTTCTTCAATTTCTCTTTCCGTAAGATTACCTC 1598
 488 CGTCAATTTACTTTTACCGTTGATTTCTTCAATTTCTCTTTCCGTAAGATTACCTC 547
 1599 TCTCTCTGTTTTTTTCTCTGCTAGATGATATATATATATATATATATATATATAT 1644
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RESULT 5
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 LOCUS BUI43512 unpublished oligo-capped cDNA library, C. elegans L1 stage
 DEFINITION Caenorhabditis elegans cDNA clone yk1196h12 3', mRNA sequence.
 ACCESSION BUI43512
 VERSION BUI43512.1 GI:18303678
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 638)
 Kohara, Y., Shin-1, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
 and Sugano, S.
 TITLE A complementary view of the C. elegans genome
 JOURNAL Unpublished (2002)
 COMMENT Contact: Tadashi Shin-1

Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.
 Location/Qualifiers
 1. 638

FEATURES

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 RNA isolated from both hermaphrodite and male N2 worms of
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 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pCR8⁺

BASE COUNT 203 a 124 c 164 g 132 t 15 others

Query Match 7.8%; Score 514.8; DB 13; Length 638;
 Best Local Similarity 89.2%; Pred. No. 6e-72; Mismatches 17; Indels 53; Gaps 1;
 Matches 579; Conservative 0; Mismatches 17; Indels 53; Gaps 1;

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 600 AGTCCGAGCAAAAGAGCCCAATCCAGAAATGCGAGGAAATACCTGTTGAAGCAGCGCT 541
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 240 GA-----CAGAT 234
 1388 CTACAAATCGGATATTCGATCTGACTTTCGCTATTTCTGCTTCGCAATTTGCTT 1447
 233 CTACAAATCGGATATTCGATCTGACTTTCGCTATTTCTGCTTCGCAATTTGCTT 174
 1448 CAACCTTCCGAGAACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 1507
 173 CAACCTTCCGAGAACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 114
 1508 TTCTTACTCGCGCCGAGCCCTGACAAATTCGTAATTTACTTTTACCGTTGATTTCTT 1567
 113 TTCTTACTCGCGCCGAGCCCTGACAAATTCGTAATTTACTTTTACCGTTGATTTCTT 54
 1568 CGATTTTCTCTTTTCCGTAAGATTACCTGCTCTGTTGTTTTTTTTT 1616
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RESULT 6	587 bp	mrna	linear	EST 24-JAN-2002
LOCUS	BJ152426			
DEFINITION	BJ152426	unpublished oligo-capped cDNA library, C. elegans L1 stage		
ACCESSION	BJ152426	Caenorhabditis elegans cDNA clone YK1307B04 3', mRNA sequence.		
VERSION	BJ152426.1	GI:18320411		
KEYWORDS	EST.			
SOURCE	Caenorhabditis elegans.			
ORGANISM	Caenorhabditis elegans.			
REFERENCE	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea			
AUTHORS	1 (bases 1 to 587)			
	Kohara, Y., Shin, I.-T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.			
TITLE	A complementary view of the C. elegans genome			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Tadasi Shin-I			
	Center For Genetic Resource Information			
	National Institute of Genetics			
	1111 Yata, Mishima, Shizuoka 411-8540, Japan			
	Tel: 81-559-81-6856			
	Fax: 81-559-81-6855			
	Email: tshini@genes.nig.ac.jp.			
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	/note="The AD-wrmcDNA library was generated with poly(A)+			
	RNA isolated from both hermaphrodite and male N2 worms of			
	all larval stages, embryos, adults and dauers and the			
	subsequent generation of cDNAs by poly(A) priming. The			
	cDNAs were cloned into pPC68"			
BASE COUNT	194 a 111 c 160 g 121 t 1 others			
ORIGIN				
Query Match	7.8%; Score 513; DB 13; Length 587;			
Best Local Similarity	91.4%; Pred. No. 1.2e-71;			
Matches 576; Conservative	0; Mismatches 1; Indels 53; Gaps 1;			
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DB	587 CGAGTGGGAAATCCGTTGGAAGCAGCGCTCCAGAATCGCCCAATCGCTCCACATCTCAC	528		
YQ	1059 CGCTTACCAAGCCAAATGATGACCTGATGCTCTCGGATTCATAGAAATCAGCGTTGGT	1118		
DB	527 CGCTTACCAAGCCAAATGATGACCTGATGCTCTCGGATTCATAGAAATCAGCGTTGGT	468		
YQ	1119 AATGCCGGAACCCCTTCTCGTGGAGGAATCGAATTCGAGTTTTCGCTGATTTGAC	1178		
DB	467 AATGCCGGAACCCCTTCTCGTGGAGGAATCGAATTCGAGTTTTCGCTGATTTGAC	408		
YQ	1179 CGCTTTGTGATTCATACGCTGAGCGGAATTCACATCGCGGTGACCGCTGTCTCAA	1238		
DB	407 CGCTTTGTGATTCATACGCTGAGCGGAATTCACATCGCGGTGACCGCTGTCTCAA	348		
YQ	1239 GATCATCATTTGCTTCCCATCATTTTTCATCTACTCTTAAGGAATTCGCTTCAAGATT	1288		
DB	347 GATCATCATTTGCTTCCCATCATTTTTCATCTACTCTTAAGGAATTCGCTTCAAGATT	288		
YQ	1299 CGATTTCGCTTAAGGAGTCAATATTTTGGACACGGTAGAGTTGAATTAATTAATTAAT	1358		
DB	287 CGATTTCGCTTAAGGAGTCAATATTTTGGACACGGTAGAGTTGAATTAATTAATTAAT	257		
YQ	1359 TGTTTTAAATTAATTAATTTTCAGATCTCAATATCGGATATCTCGTATCTGGACTT	1418		

QY	1419	TCGGCATATTCGTCGTCGCATTCGTCCTTCAACTTCCTTCCGACAGAACAGACAGAACT	1478
Db	220	TGGGCAATTCCTGCTGCTGCCCATTCGTCCTTCAACTTCCTTCCGACAGAACAGACAGAACT	161
QY	1479	GCTTAGGACAGAGAGCTCCGCTTCTTTTCTTACTCCGCCACAGCCCTGCAGAAATTC	1538
Db	160	GCTTAGGACAGAGAGCTCCGCTTCTTTTCTTACTCCGCCACAGCCCTGCAGAAATTC	101
QY	1539	CGCATTAATTCCTTCAACGTCGATTCCTTCATTTCTCTCTTTTCCGTAGATTTACCTC	1598
Db	100	CGTCATTAATTCCTTCAACGTCGATTCCTTCGATTTCTCTCTTTTCCGTAGATTTACCTC	41
QY	1599	TCCTCTGCTTTTCTTTTCTCTGTCAGAA	1628
Db	40	TCCTCTGCTTTTCTTTTCTCTGTCAGAA	11
RESULT 7			
LOCUS	AU215190/c	556 bp	mRNA linear EST 17-JUL-2001
DEFINITION	AU215190	unpublished oligo-capped cDNA library, stage L2	
ACCESSION	Caenorhabditis elegans cDNA clone	yk822e10 3', mRNA sequence.	
VERSION	AU215190		
KEYWORDS	AU215190.1	GI:14853347	
SOURCE	EST.		
ORGANISM	Caenorhabditis elegans.		
REFERENCE	Caenorhabditis elegans.		
AUTHORS	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae		
	; Rhabditidae; Pelodiderinae; Caenorhabditis.		
	1 (bases 1 to 556)		
	Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.		
	and Sugano,S.		
TITLE	A complementary view of the C. elegans genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Yuji Kohara		
	Genome Biology Lab.		
	National Institute of Genetics		
	Yata 111, Mishima, Shizuoka 411, Japan		
	Tel: 81-559-81-6854		
	Fax: 81-559-81-6855		
	Email: ykohara@lab.nig.ac.jp.		
FEATURES	Location/Qualifiers		
source	1..556		
	/organism="Caenorhabditis elegans"		
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	/sex="Hermaphrodite"		
	/tissue_type="whole animal"		
	/dev_stage="L2"		
	/note="The AD-wrmcDNA library was generated with poly(A)+		
	RNA isolated from both hermaphrodite and male N2 worms of		
	all larval stages, embryos, adults and dauvers and the		
	subsequent generation of cDNAs by poly(A) priming. The		
	cDNAs were cloned into pPC86"		
BASE COUNT	157 a 114 c 158 g 127 t		
ORIGIN			
Query Match	7.2%; Score 473.4; DB 9; Length 556;		
Best Local Similarity	90.9%; Pred. No. 2.3e-65;		
Matches 537; Conservative	0; Mismatches 1; Indels 53; Gaps 1;		
QY	968	AGTCGAGGCAAAACCCCAATCCAGAGGTCGATGGAGTAATCTGTGAAGACAGCGT	1027
Db	538	AGTCGAGGCAAAACCCCAATCCAGAGGTCGATGGAGTAATCTGTGAAGACAGCGT	479
QY	1028	CCAAGATGCGCCCAATGCTGCACATCTCCACGCTACACAGCAATATTGACCTGGATGC	1087

Db	478	CCAAGAAATCGCCCAATCGCTCCACATCTCAGCGCTCTACAGGACCAACAATTGACCTGGATGC	419
Oy	1088	TCCTCGGATTCCATNAGAAATCAGCGGTTGTGTAAATGCGCCGGAACCCCTTCCTCGGGAGGAA	1147
Db	418	TCCTCGGATTCCATNAGAAATCAGCGGTTGTGTAAATGCGCCGGAACCCCTTCCTCGGGAGGAA	359
Oy	1148	TCGGATTCGCGAGTTTTCGCCCTTGATTTCAACCGCTTTTGTGGAATTTTCATCCGTAAGCTGGA	1207
Db	358	TCGGATTCGCGAGTTTTCGCCCTTGATTTCAACCGCTTTTGTGGAATTTTCATCCGTAAGCTGGA	299
Oy	1208	ACTTACCATGCGCGGTGACCGCGTGTCTTCAAGTACATCATTCGTTCCCATATTTTC	1367
Db	298	ACTTACCATGCGCGGTGACCGCGTGTCTTCAAGTACATCATTCGTTCCCATATTTTC	239
Oy	1268	ATACCTTAAAGGAAATTCGCTTCTTAGATTCGATTTGGCTTAAGGAGTCATTAATGTTG	1327
Db	238	ATACCTTAAAGGAAATTCGCTTCTTAGATTCGATTTGGCTTAAGGAGTCATTAATGTTG	179
Oy	1328	GACAGGTAGGAGTGAATTAATTATTAATTGAATTTTAAATAATTAATTTTCAGAT	1387
Db	178	GA-----CAGAT	172
Oy	1388	CTACCAATTCGGATATCTCGTATCTGGAATTCCTGGCTATTCCTGCTCGCATTTGCTT	1447
Db	171	CTACCAATTCGGATATCTCGTATCTGGAATTCCTGGCTATTCCTGCTCGCATTTGCTT	112
Oy	1448	CAACTTTCGCCAGAACAGACAGACAAAGAAGCTGCCAAGGACAGAGTGCCTCGCTCTTTT	1507
Db	111	CAACTTTCGCCAGAACAGACAGACAAAGAAGCTGCCAAGGACAGAGTGCCTCGCTCTTTT	52
Oy	1508	TTCTTACTCGGCCCGACCGCTCGACAAATTCCTGTCATTTACTTTACCGT	1558
Db	51	TTCTTACTCGGCCCGACCGCTCGACAAATTCCTGTCATTTACTTTACCGT	1

RESULT 8
 BUI34935/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

BUI34935 562 bp mRNA linear EST 23-JAN-2002
 BUI34935 unpublished oligo-capped cDNA library, *C. elegans* L1 stage.
 Caenorhabditis elegans cDNA clone yk1094.c02 3', mRNA sequence.
 BUI34935
 BUI34935
 BUI34935.1 GI:18295092
 EST.
 Caenorhabditis elegans.
 Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Pelodierinae; Caenorhabditis.
 1 (bases 1 to 562)
 Kohara,Y., ShIn-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
 and Sugano,S.
 A complementary view of the *C.elegans* genome
 Unpublished (2002)
 Contact: Tadasu Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel.: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 location/Qualifiers

FEATURES
 source
 1..562 name="Caenorhabditis elegans"

BASE COUNT	187	a	103	c	155	g	114	t	3	others
ORIGIN	subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"									

Query Match	7.2%;	Score 470.8;	DB 13;	Length 502;
Best Local Similarity	Pred. No. 5.8e-65;			
Matches 546;	conservative	0;	Mismatches 5;	Indels 54;
				Gaps 2

QY	1025	GGTCGCAAAATCGGCCAATGCGCTCCACATCTCACCGCTACGCGT	1144
Db	562	GCTCCAAATCGCCCAATCGCTCCACATCGACCGCTACGCGCAATGACCTGGA	503
QY	1085	TGCTCTCGGAAATTCATGATCAGCGGTGTGTAAATGCGCGGAACCTCTCGTGGAG	1144
Db	502	TGCTCTCGGAAATTCATGATCAGCGGTGTGTAAATGCGCGGAACCTCTCTGTGGAG	443
QY	1145	GAATCGGATTCGCATCTTTTGGCCGCTTCATTTACACCGCTTTTGGAAATTCATCCGTAGCT	1204
Db	442	GAATCGGATTCGCCAATTTTGGCCGCTTCATTTACACCGCTTTTGGAAATTCATCCGTAGCT	383
QY	1205	GGAACTTACATCGCGCGGTGACCGCTGTCTTCAAGTACATCATTGCTTTCCCATATTT	1264
Db	382	GGAACTTACATCAGCGCGGTGACCGCTGTCTTCAAGTACATCATTGCTTTCCCATATTT	323
QY	1265	TCCATCTCTTAAAGGAATTCGCTCTTAAGATTCGATTTGGCTAAAGGAGTCATTAATG	1324
Db	322	TCCATCTCTTAAAGGAATTCGCTCTTAAAGATTCGATTTGGTAAAGGAGTCATTAATG	263
QY	1325	TTTGACAGTAGGAGTGTGAATTTAATTTAATTTGTTTAAATTTAAATTTAATTTTCA	1384
Db	262	TTTGGA-----CA 256	
QY	1385	GATCTACAAATTCGGGATATCTGTATCTGTGACTTTCGGCTATTTCTGTCTCGGCATTTG	1444
Db	255	GATCTACAAATTCGGGATATCTGTATCTGTGACTTTCGGCTATTTCTGTCTCGGCATTTG	196
QY	1445	CTTCAACTCTTGGCAGAAACAAGACAAAGAAGCTGCTTAGAGACAGAGATGTCGCGCTCT	1504
Db	195	CTTCAACTCTTGGCAGAAACAAGACAAAGAAGCTGCTTAGAGACAGAGATGTCGCGCTCT	136
QY	1505	TTTTTCTTACTCGCGCCACAGCCTCAACAATTCGTGCAATTTACTTTTACCGTGAATTT	1564
Db	135	TTTTTCTTACTCGCGCCACAGCCTCAACAATTCGTGCAATTTACTTTTACCGTGAATTT	76
QY	1565	CTTGGATTTCTCTTTTCCGTAGATTTAACCTCTCTCT-CTCGATTTTCTTCTCTCTC	1623
Db	75	CTTGGATTTCTCTTTTCCGTAGATTTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	16
QY	1624	TAGAA 1628	
Db	15	TAGAA 11	

RESULT 9	
BIJ07235	606 bp mRNA linear EST 23-JAN-2002
LOCUS	
DEFINITION	Caenorhabditis elegans C. elegans L1 stage
ACCESSION	Bj107235
VERSION	Bj107235.1
KEYWORDS	GI:18267260
SOURCE	EST
ORGANISM	Caenorhabditis elegans.
	Caenorhabditis elegans.
	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
	; Rhabditidae; Pelodermidae; Caenorhabditis.
	1 (bases 1 to 606)
REFERENCE	Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
AUTHORS	and Sugano,S.
TITLE	A complementary view of the C.elegans genome
JOURNAL	Unpublished (2002)
COMMENT	Contact: Tadasu Shin-i
	Center For Genetic Resource Information

National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshimigene.nig.ac.jp.

FEATURES
Source
Location/Qualifiers

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/dev_stage="L1"
/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
BASE COUNT 136 a 166 c 131 g 173 t
ORIGIN

Query Match
Best Local Similarity 90.2%; Score 433.4; DB 13; Length 606;
Matches 497; Conservative 0; Mismatches 1; Indels 53; Gaps 1;

QY 968 AGTCCGAGCAAGAGCCCAATCCAGAACTGCGATGGAATACCTGTGAAGCAGCGCT 1027
DB 109 AGTCCGAGCAAGAGCCCAATCCAGAACTGCGATGGAATACCTGTGTGAAGCAGCGCT 168
QY 1028 CCAGAGATGCGCCCAATCGCTCCACATCTCACCCTTACACGACCAATTCCTGATGC 1087
DB 169 CCAGAGATGCGCCCAATCGCTCCACATCTCACCCTTACACGACCAATTCCTGATGC 228
QY 1088 TCTCCGATTCAGAAATCAACGCGTGTGAATGCGCGAAGCCCTCTCGCGAGAA 1147
DB 229 TCTCCGATTCAGAAATCAACGCGTGTGAATGCGCGAAGCCCTCTCGCGAGAA 288
QY 1148 TCGGATTCGCAATTTGGCGCTTCCATTCACCGCTTTGTGGATTCATCCGATGGA 1207
DB 289 TCGGATTCGCAATTTGGCGCTTCCATTCACCGCTTTGTGGATTCATCCGATGGA 348
QY 1208 ACTTACATGCGCGGTGACCGCTGCTTCAAGTACATCATCTGTTCCCATATTTTC 1267
DB 349 ACTTACATGCGCGGTGACCGCTGCTTCAAGTACATCATCTGTTCCCATATTTTC 408
QY 1268 ATACTCTTAAGGAAATTCGCTTCTTGAATTCGATTTGGCTAAGGAGTCAATATGTTG 1327
DB 409 ATACTCTTAAGGAAATTCGCTTCTTGAATTCGATTTGGCTAAGGAGTCAATATGTTG 468
QY 1328 GACAGTAGAGTGAATTAATTATTTAAATTAATTAATTAATTTTCAGAT 1387
DB 469 GA-----CAGAT 475
QY 1388 CTACAATCGGGAATTCGTATCTGACTTGGCTATTTCTCTCGCATTTGCT 1447
DB 476 CTACAATCGGGAATTCGTATCTGACTTGGCTATTTCTCTCGCATTTGCT 535
QY 1448 CAACCTTTCGACAGACAGCAAGAGTCTGCTAGGACAGATGCTCGCCTCTTTT 1507
DB 536 CAACCTTTCGACAGACAGCAAGAGTCTGCTAGGACAGATGCTCGCCTCTTTT 595
QY 1508 TTCTTACTCGG 1518
DB 596 TTCTTACTCGG 606

RESULT 10
AU203561 515 bp mRNA linear EST 17-JUL-2001
LOCUS AU203561
DEFINITION AU203561 unpublished oligo-capped cDNA library, stage L2

ACCESSION
AU203561
VERSION
AU203561.1 GI:14834309
KEYWORDS
EST.
SOURCE
ORGANISM
Caenorhabditis elegans.

REFERENCE
AUTHORS
Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.

TITLE
JOURNAL
COMMENT
A complementary view of the C. elegans genome
Unpublished (2001)
Contact: Yuji Kohara
Genome Biology Lab.

National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers

1.515
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/db_xref="taxon:6239"
/clone="yk822e10"
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/dev_stage="L2"

BASE COUNT 115 a 135 c 117 g 145 t 3 others
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Query Match
Best Local Similarity 99.7%; Score 365.4; DB 9; Length 515;
Matches 366; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 968 AGTCCGAGCAAGAGCCCAATCCAGAACTGCGATGGAATACCTGTGAAGCAGCGCT 1027
DB 122 AGTCCGAGCAAGAGCCCAATCCAGAACTGCGATGGAATACCTGTGAAGCAGCGCT 181
QY 1028 CCAGAGATGCGCCCAATCGCTCCACATCTCACCCTTACACGACCAATTCCTGATGC 1087
DB 182 CCAGAGATGCGCCCAATCGCTCCACATCTCACCCTTACACGACCAATTCCTGATGC 241
QY 1088 TCTCCGATTCAGAAATTCGCTTCTTGAATTCGATTTGGCTAAGGAGTCAATATGTTG 1147
DB 242 TCTCCGATTCAGAAATTCGCTTCTTGAATTCGATTTGGCTAAGGAGTCAATATGTTG 301
QY 1148 TCGGATTCGCAATTTGGCGCTTCCATTCACCGCTTTGTGGATTCATCCGATGGA 1207
DB 302 TCGGATTCGCAATTTGGCGCTTCCATTCACCGCTTTGTGGATTCATCCGATGGA 361
QY 1208 ACTTACATGCGCGGTGACCGCTGCTTCAAGTACATCATCTGTTCCCATATTTTC 1267
DB 362 ACTTACATGCGCGGTGACCGCTGCTTCAAGTACATCATCTGTTCCCATATTTTC 421
QY 1268 ATACTCTTAAGGAAATTCGCTTCTTGAATTCGATTTGGCTAAGGAGTCAATATGTTG 1327
DB 422 ATACTCTTAAGGAAATTCGCTTCTTGAATTCGATTTGGCTAAGGAGTCAATATGTTG 481
QY 1328 GACAGAT 1334
DB 482 GACAGAT 488

RESULT 11

LOCUS	BJ103911	502 bp	mrna	linear	EST 18-JAN-2002
DEFINITION	BJ103911	unpublished oligo-capped cDNA library, <i>C. elegans</i> L1 stage			
ACCESSION	Caenorhabditis elegans cDNA clone YK1055904 5',				mrna sequence.
VERSION	BJ103911				
KEYWORDS	BJ103911.1	GI:18246581			
SOURCE	EST.				
ORGANISM	Caenorhabditis elegans.				
	Euarchyot, Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabditoidea				
	; Rhabditidae; Pelodermidae; Caenorhabditis.				
REFERENCE	1 (bases 1 to 502)				
AUTHORS	Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.				
	and Sugano, S.				
	A complementary view of the <i>C. elegans</i> genome				
	unpublished (2002)				
TITLE	Contact: Tadasu Shin-i				
JOURNAL	Center For Genetic Resource Information				
COMMENT	National Institute Of Genetics				
	1111 Yata, Mishima, Shizuoka 411-8540, Japan				
	Tel: 81-559-81-6856				
	Fax: 81-559-81-6855				
	Email: tsnini@genes.nig.ac.jp.				
FEATURES	Location/Qualifiers				
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	organism="Caenorhabditis elegans"				

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/dev_stage="L1"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauvers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT      160 a      99 c      103 g      139 t      1 others
ORIGIN

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Matches 341;	Conservative	0;	Mismatches 9;	Indels 1;	Gaps 1
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Db 147	AAAGATCTCTGACCCCGATGACAGAGTCCGCTCAATGCAATCGAACAAAGAGGAG	206			
OY 5544	TTCTCACTTACCGGATCCGAGACGAGATCACCTCAATCTCTCCATACCTCATTAATACC	5603			
Db 207	TTCTCACTTACCGGATCCGAGACGAGATCACCTCAATCTCTCCATACCTCATTAATACC	266			
OY 5604	CACACCTGCACAGTGAAGAAAGCCGATCCAGACGCGTTTCAGAGTATTTGATTCGAAG	5663			
Db 267	CACACCTGCACAGTGAAGAAAGCCGATCCAGACGCGTTTCAGAGTATTTGATTCGAAG	326			
OY 5664	GAGAAAGTCGGTGAACCTATGATATGACATACGTCACCTTGATATTTCTTCGCTAAA	5723			
Db 327	GAGAAAGTCGGTGAACCTATGATATGACATACGTCACCTTGATATTTCTTCGCTAAA	386			
OY 5724	GACAAGAGAGATGCTAAGAAAAATGTTTTTTTGGTTGGTTGGTGGTGGAGGAG	5783			
Db 387	GACAAGAGAGATGCTAAGAAAAATGTTTTTTTGGTTGGTTGGTGGTGGAGGAG	445			
OY 5784	GACCTTCACTCTTTTAATTCACATAACATATGGAAAAACCGTTGAAA	5834			
Db 446	GACCTTCACTCTTTTAATTCACATAACATATGGAAAAACCGTTGAAA	496			

RESULT 12
AU202666

LOCUS	AU202666	501 bp	mRNA	linear	EST 17-JUL-2001
DEFINITION	AU202666 unpublished oligo-capped cDNA library, stage L2				
ACCESSION	Caenorhabditis elegans cDNA clone YK811C04 5', mRNA sequence.				
VERSION	AU202666				
KEYWORDS	AU202666.1	GI:14832634			
SOURCE	EST.				
ORGANISM	Caenorhabditis elegans.				
	Caenorhabditis elegans				
	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;				
	; Rhabditidae; Peloiderinae; Caenorhabditis.				
REFERENCE	1 (bases 1 to 501)				
AUTHORS	Kohara,Y., Shun-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.				
	and Sugano,S.				
TITLE	A complementary view of the C.elegans genome				
JOURNAL	unpublished (2001)				
COMMENT	Contact: Yuji Kohara				
	Genome Biology lab.				
	National Institute of Genetics				
	Yata 1111, Mishima, Shizuoka 411, Japan				
	Tel: 81-559-81-6854				
	Fax: 81-559-81-6855				
FEATURES	Email: ykohara@lab.nig.ac.jp.				
	location/Qualifiers				
Source	1..501				
	/organism="Caenorhabditis elegans"				

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/origins="N2"
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/dev_stage="L2"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pC86"
BASE COUNT      161 a      100 c      102 g      138 t
ORIGIN

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Query Match	Best Local Similarity	4.9%;	Score 323;	DB 9;	Length 501;
Matches 340;	Conservative	0;	Mismatches 10;	Indels 1;	Gaps 1;
QY 5484	AAATTTTCAGGTGACCCCGATGACAGAGTGGCGCTTCATGCAATGGAACAAAGAGGAG	5543			
Db 148	AAAGATACCTGTGACCCCGATGACAGAGTGGCGCTTCATGCAATGGAACAAAGAGGAG	207			
QY 5544	TTTCACCTTACCGGATCGAGCAGAGATCACCTTAATCTCTGCATACCTCATATATACC	5603			
Db 208	TTTCACCTTACCGGATCGAGCAGAGATCACCTTAATCTCTGCATACCTCATATATACC	267			
QY 5604	CACACTGCAAGTGAAGAAAGCCCGATGCAAGCGTGTTCAGAGTATTTGATTCAAAG	5663			
Db 268	CACACTGCAAGTGAAGAAAGCCCGATGCAAGCGTGTTCAGAGTATTTGATTCAAAG	327			
QY 5664	GAGAAGATCGGTGAAGACTATGATATGACATACGTACTCTTGATATCTTTCCGCTAAA	5723			
Db 328	GAGAAGATCGGTGAAGACTATGATATGACATACGTACTCTTGATATCTTTCCGCTAAA	387			
QY 5724	GACAAGGAGAGTGTCAAGAAATGTTTTTTTGTGGTTGGTTGGTGAAGGAG	5783			
Db 388	GACAAGGAGAGTGTCTAAGAAATGTTTTTTTGTGTTGTTGCTTTGTTTGAAGGAG	446			
QY 5784	GACTTTCATCTCTTTTAATTCACAATTAACATATGGAACCGGTGAA	5834			
Db 447	GACTTTCATCTCTTTTAATTCACAATTAACATATGGAACCGGTGAA	497			

RESULT 13			
BJ114579			
LOCUS	BJ114579	502 bp	mRNA linear EST 23-JAN-2002

BASE COUNT
ORIGIN

161 a	100 c	102 g	139 t
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Query Match	Best Local Similarity	4.98;	Score 323;	DB 13;	Length 502;
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Matches 340;	Conservative	0;	Mismatches 10;	Indels	1;
QY 5484	AATTTTCCAGTCGACCCCGATGCAAGCTCGCTCAATGCATCGACAAGAAAGAGAG	5543			
Db 147	AAAGATACTCTCGACCCCGATGCAAGCTCGCTCAATGCATCGACAAGAAAGAGAG	5543			
QY 5544	TTCTCACTTACCGGATCCGACGACGAGATCACCCTCAATCTCCATACCTCATATACC	5603			
Db 207	TTCTCACTTACCGGATCCGACGACGAGATCACCCTCAATCTCCATACCTCATATACC	5603			
QY 5604	CACAACTGCAACGTAAGAAAGCCGGATGCAAGCGGTTTCAGATATTGATTCCAAAG	5663			
Db 267	CACAACTGCAACGTAAGAAAGCCGGATGCAAGCGGTTTCAGATATTGATTCCAAAG	5663			
QY 5664	GAGAAATCGGTGGAACCTATGATGACATCGTCACTCTTGATTAATCTTCGCTAA	5723			
Db 327	GAGAAATCGGTGGAACCTATGATGACATCGTCACTCTTGATTAATCTTCGCTAA	5723			
QY 5724	GACAAGAGAAAGTCGTACGAAAAATGTTTTTTGTTGGTTGGTTGTTGGAAGGAG	5783			
Db 387	GACAAGAGAAAGTCGTACGAAAAATGTTTTTTGTTGGTTGGTTGTTGGAAGGAG	5783			
QY 5784	GACTTCTATCTCTTTTAATCAACAATAAAGCTATGGAAGCCGTTGAAA	5834			
Db 446	GACTTCTATCTCTTTTAATCAACAATAAAGCTATGGAAGCCGTTGAAA	5834			

BASE COUNT 156 a 100 c 102 g 138 t 4 others
ORIGIN

Query Match	Similarity	4.9%	Score 322.4	DB 13	Length 500
Best Local Similarity	98.0%		Pred. No. 1.9e-41		
Matches 337	Conservative	0	Mismatches	6	Indels 1; Gaps 1
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DB	327	GAGAAATCGGTGGAACCTATGATATGACATACGTCACCTTGATATCTTCGGCTAA	386		
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LOCUS	AV190122	360 bp	mRNA	linear	EST 22-JUL-1999
DEFINITION	AV190122 Yuiji Kohara unpublished cDNA,Strain N2 hermaphrodite embryo <i>Caenorhabditis elegans</i> cDNA clone yk567b11 5', mRNA				

Thu Mar 6 08:14:03 2003

us-09-993-420a-1.rst

Page 10

sequence.
ACCESSION AV190122 GI:5572105
VERSION AV190122.1
KEYWORDS EST
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara, Y., Shin, I., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H., Nishigaki, A., Motohashi, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, T. and Nomoto, H.
TITLE Expressed genes in C. elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
location/Qualifiers
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BASE COUNT 80 a 105 c 78 g 97 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 968 AGTCGAGGCAAGAGCGCCATCCAGAGTTCGATGGGAAATACCTGTGAGAGCAGCGCT 1027
DB 43 AGTCGAGGCAAGAGCGCCATCCAGAGTTCGATGGGAAATACCTGTGAGAGCAGCGCT 102
QY 1028 CCAAGAAATCGCCCAATCGCTCCACATCTACCGTCTACCGCACAATGACCTGGATGC 1087
DB 103 CCAAGAAATCGCCCAATCGCTCCACATCTACCGTCTACCGCACAATGACCTGGATGC 162
QY 1088 TCTCCGATTCCTAAGATCAGGCGTGTGTATGCGCGGAACCTTCTCGTGGAGGAA 1147
DB 163 TCTCCGATTCCTAAGATCAGGCGTGTGTATGCGCGGAACCTTCTCGTGGAGGAA 222
QY 1148 TCGGATTCGAGTTTGGCCGTTGATTCACCGCTTTTGGATTCATCCGTAAGCTGGA 1207
DB 223 TCGGATTCGAGTTTGGCCGTTGATTCACCGCTTTTGGATTCATCCGTAAGCTGGA 282
QY 1208 ACTTACCATGCGGCTGACCGGTGTCTCAAGTACATCATTTGCTTCCCATTTTCC 1267
DB 283 ACTTACCATGCGGCTGACCGGTGTCTTCAAGTACATCATTTGCTTCCCATTTTCC 342
QY 1268 ATACTTTAAGGAATTC 1285
DB 343 ATACTTTAAGGAATTC 360

Search completed: February 28, 2003, 04:28:38
Job time : 7971.47 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 18:37:30 ; Search time 3219.62 Seconds

(without alignments)
11886.551 Million cell updates/sec

Title: US-09-993-420A-2

Perfect score: 1315

Sequence: 1 tttagatgacacgacgcgcac.....cgttcaaaaaaaaaaaaaa 1315

Scoring table: IDENTITY NUC

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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13: gb_un:*
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15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
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21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_luv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pin:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hgo_hum:*
40: em_hgo_mus:*
41: em_hgo_other:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	632.6	48.1	7035	3	CELCYT1A	L26545 Caenorhabdi
2	632.6	48.1	33477	3	CECT07C4	Z29443 Caenorhabdi
3	177.4	13.5	3419	3	CELCBHO	L26546 Caenorhabdi
4	81.8	6.2	7218	6	I66494	I66494 Sequence 14
5	55.6	4.2	7218	6	I66494	I66494 Sequence 14
6	54.6	4.2	146383	2	AC116367	AC116367 Oryza sat
7	50.8	3.9	167264	2	AC095776	AC095776 Rattus no
8	47.6	3.6	289	6	ARI62089	ARI62089 Sequence
9	47.6	3.6	289	6	ARI66514	ARI66514 Sequence
10	46.6	3.5	107731	9	AC005476	AC005476 Homo sapi
11	46.4	3.5	136551	2	AC048354	AC048354 Homo sapi
12	46.4	3.5	229422	2	AC097544	AC097544 Homo sapi
13	45.8	3.5	242336	2	AC097416	AC097416 Rattus no
14	45.4	3.5	170005	2	AC106291	AC106291 Rattus no
15	45.2	3.4	101509	2	AC027353	AC027353 Homo sapi
16	45	3.4	88827	2	AC103497	AC103497 Rattus no
17	44.8	3.4	96102	8	F22D1	AF296834 Arabidops
18	44	3.3	151663	2	AC102402	AC102402 Mus muscu
19	44	3.3	170047	2	AC091947	AC091947 Homo sapi
20	43.6	3.3	220114	2	AL731767	AL731767 Mus muscu
21	43.2	3.3	95892	2	AC103202	AC103202 Rattus no
22	43.2	3.3	250733	2	AC106312	AC106312 Rattus no
23	42.8	3.3	143301	2	AC095156	AC095156 Rattus no
24	42.8	3.3	193067	2	AC115546	AC115546 Rattus no
25	42.8	3.3	200885	2	AC119856	AC119856 Mus muscu
26	42.4	3.2	124257	2	AC120269	AC120269 Rattus no
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28	42.4	3.2	153635	2	AC122103	AC122103 Rattus no
29	42.4	3.2	180889	2	AC079986	AC079986 Homo sapi
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32	42.2	3.2	125020	9	AF429315	AF429315 Homo sapi
33	42.2	3.2	142142	2	AC091173	AC091173 Homo sapi
34	42.2	3.2	186676	9	AC067881	AC067881 Homo sapi
35	42.2	3.2	215528	2	AC099105	AC099105 Rattus no
36	42	3.2	3280	3	AF069757	AF069757 Dictyoste
37	42	3.2	35409	3	CEC44C10	Z69787 Caenorhabdi
38	42	3.2	118800	2	AC130445	AC130445 Rattus no
39	42	3.2	166197	2	AC114704	AC114704 Rattus no
40	41.8	3.2	224312	2	AL606969	AL606969 Mus muscu
41	41.6	3.2	2811	8	ATAPRTGEN	X96867 A.thaliana
42	41.6	3.2	115666	2	AC105744	AC105744 Oryza sat
43	41.6	3.2	116905	8	AC009322	AC009322 Arabidops
44	41.6	3.2	198289	2	AC113023	AC113023 Mus muscu
45	41.6	3.2	199239	2	AC093370	AC093370 Mus muscu

ALIGNMENTS

RESULT 1
LOCUS CELCYT1A 7035 bp DNA linear INV 22-APR-2002
DEFINITION Caenorhabditis elegans CYT-1 (cyt-1) and CED-9 (ced-9) genes,
complete cds; and unknown gene.
ACCESSION L26545
VERSION L26545
KEYWORDS L26545.1 GI:433174

SOURCE
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
1 (bases 1 to 7035)
Hengartner,M.O. and Horvitz,H.R.
C. elegans cell survival gene ced-9 encodes a functional homolog of


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CDNA EST YK318c1.5 comes from this gene
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CDNA EST YK381f5.3 comes from this gene
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QY	849	ACGATTTCAATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	908
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JOURNAL TITLE	Direct Submission
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 167264)
TITLE	Worley,K.C.
JOURNAL	Direct Submission
REFERENCE	Submitted (17-SEP-2001)
AUTHORS	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
TITLE	3 (bases 1 to 167264)
REFERENCE	Worley,K.C.
AUTHORS	Direct Submission
JOURNAL	Submitted (11-JUL-2002)
REFERENCE	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT	On Jul 10, 2002 this sequence version replaced gi:20975899.

Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Huylk,S., Hunne,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jollivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureishi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louisedg,H., Lozado,W.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Mattin,R., Martindale,A., Martinez,E., Massey,E., Maxhiney,E., McLeod,M.P., Medor,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,S., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nockenhov,S., Ogum,M., Okunonu,G., Ogunyeye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojndahan,I., Rolfe,M., Ruiz,S., Savery,G., Scheer,S., Scott,G., Shen,H., Shoobhat,N., Sisson,I., Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabori,P., Tameris,N., Tameris,K., Tang,H., Tansal,K., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S., Williams,G., Williamson,A., Wleczek,R., Wooten,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G., and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 167264)
2 (bases 1 to 167264)
Worley,K.C.

Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 167264)
Worley,K.C.

Direct Submission
Submitted (11-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 10, 2002 this sequence version replaced gi:20975899.

Genome Center
Center: Baylor College of Medicine
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GDHN
Center clone name: CH230-9K20
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 99661 bases at least Q40
Consensus quality: 104971 bases at least Q30
Consensus quality: 108925 bases at least Q20

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
NOTE: This is a working draft sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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1109 1208: gap of unknown length
1209 2405: contig of 1197 bp in length
2406 2505: gap of unknown length
2506 3645: contig of 1140 bp in length
3646 3745: gap of unknown length
3746 5337: contig of 1592 bp in length

*	63591	65170: contig of 1580 bp in length
*	65171	65270: gap of unknown length
*	65271	66442: contig of 1172 bp in length
*	66443	66542: gap of unknown length
*	66543	68996: contig of 2454 bp in length
*	68997	69096: gap of unknown length
*	68997	70506: contig of 1410 bp in length
*	70507	70606: gap of unknown length
*	70607	72573: contig of 1967 bp in length
*	72574	72673: gap of unknown length
*	72674	74815: contig of 2142 bp in length
*	74816	74915: gap of unknown length
*	74916	76935: contig of 2020 bp in length
*	76936	77035: gap of unknown length
*	77036	78940: contig of 1905 bp in length
*	78941	79040: gap of unknown length
*	79041	81642: contig of 2602 bp in length
*	81643	81742: gap of unknown length
*	81743	84154: contig of 2412 bp in length
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*	85898	89530: contig of 3633 bp in length
*	89531	89630: gap of unknown length
*	89631	92433: contig of 2803 bp in length
*	92434	92533: gap of unknown length
*	92534	95170: contig of 2637 bp in length

Query Match		3.9%; Score 50.8; DB 2; Length 167264;
Best Local Similarity	48.6%;	Pred. No. 0.01;
Matches 103; Conservative	0;	Mismatches 109; Indels 0; Gaps 0;
OY 1104	TTTTCTGCGCCGTGGCCTTAAGCTCCCGCTTCTCTTCACATTTCCAAATAACCCTGTATC	1163
Dd 999	TTTCTGTCTGCCCGCCCCCGCCGCCCGNNNNAAAAACCNNTAANAANANTWTT	940
OY 1164	TCAATATTCACTTCTCACCTTAACGTGTCCTTGTCGTGCGCTCTTCCAACCTCCCCCA	1223
Dd 939	TNNTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCCCCCCCCCCCCCCNN	880
OY 1224	AATTCTGTACGCGTAGCGCATTTGTATTTATTTTTTTTCAAATTTGTTCTCTCTACAA	1283
Dd 879	CCCCCCCCCCCCCCCCNNNNNNNNNNNTTTTTTTTTTTTTTTTTTTTATTTTTTTTAT	820
OY 1284	CACCAAAAAAACGGTTCACAAAAAATAAAAAA	1315
Dd 819	AAAAAAAAAAAAAAAAAAAAAAAAAAAAACA	788
RESULT 8		
ARI62089/c		
LOCUS	Sequence 17 from patent US 6258558.	289 bp DNA linear PAT 17-OCT-2001
DEFINITION	ARI62089	
ACCESSION	ARI62089.1	GI:16229155
VERSION		
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 289)	
TITLE	Szostak,J.W., Roberts,R.M. and Liu,R.	
JOURNAL	Method for selection of proteins using RNA-protein fusions	
FEATURES	Patent: US 6258558-A 17 10-JUL-2001;	
source	Location/Qualifiers	
	1..289	
BASE COUNT	41 a 13 c 9 g 15 t	211 others
ORIGIN	/organism="unknown"	
Query Match	3.6%; Score 47.6; DB 6; Length 289;	
Best Local Similarity	11.7%;	Pred. No. 0.03;
Matches 32; Conservative	107;	Mismatches 135; Indels 0; Gaps 0;

FEATURES	end is at base position 14951 of RP6-91H8.
source	Location/Qualifiers
repeat_region	1. .107731 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="14" /map="14q24.3" /clone="RP1-261D10" /clone_lib="RRC1-1" 1. .94
repeat_region	/rpt_family="Alu" 140. .430
repeat_region	/rpt_family="Alu" 629. .704
repeat_region	/rpt_family="L2" 1144. .1428
repeat_region	/rpt_family="Alu" 1433. .1462
repeat_region	/rpt_family="(CAGA)n" 1514. .1570
repeat_region	/rpt_family="MIR" 1610. .1786
misc_feature	/rpt_family="MIR" 2029. .2267
repeat_region	/note="match to EST AI940527 (NID:95687508)" 2591. .2710
repeat_region	/rpt_family="L2" 3552. .3686
repeat_region	/rpt_family="L1" 3687. .4002
repeat_region	/rpt_family="Alu" 4003. .4499
repeat_region	/rpt_family="L1" 5052. .5288
repeat_region	/rpt_family="Alu" 5469. .5586
repeat_region	/rpt_family="MIR" 6139. .6227
repeat_region	/rpt_family="MIR" 6343. .6652
repeat_region	/rpt_family="Alu" 6967. .7278
repeat_region	/rpt_family="Alu" 7360. .7460
repeat_region	/rpt_family="MER1_type" 8048. .8292
repeat_region	/rpt_family="Alu" 8293. .8656
repeat_region	/rpt_family="MIR" 8657. .8720
repeat_region	/rpt_family="Alu" 9506. .9793
repeat_region	/rpt_family="L1" 10691. .10988
repeat_region	/rpt_family="Alu" 11719. .11849
repeat_region	/rpt_family="MIR" 11847. .12299
repeat_region	/rpt_family="L2" 12386. .12428
repeat_region	/rpt_family="MIR" 13243. .13270
repeat_region	/rpt_family="(TGAAG)n" 13547. .13572
repeat_region	/rpt_family="AT-rich" 13689. .13795
repeat_region	/rpt_family="L2" 14137. .14165
repeat_region	/rpt_family="(TTTTTG)n" 14683. .15198
repeat_region	/rpt_family="L1" 14969. .14971
misc_feature	/note="similar to EST AA148730 (NID:91719241) z144a10.s1"

	misc_feature	15222..15792	/note="similar to EST AA411589 (NID:g2069122) zv30903.r1"
	misc_feature	15222..15372	/note="similar to EST AA853596 (NID:g2940335)"
	misc_feature	15231..15735	/note="similar to Mus musculus EST AA986226 (NID:g31367550)
	misc_feature	uc73g05.y1"	
	misc_feature	15239..15718	/note="similar to EST AA147161 (NID:g1716536) z032f01.r1"
	misc_feature	15251..15863	/note="similar to Mus musculus EST AA656594 (NID:g2592748)
	misc_feature	vs26b07.i1	
	misc_feature	15379..15826	/note="similar to Mus musculus EST AA655551 (NID:g2591705)
	misc_feature	vs42d08.r1"	
	misc_feature	15380..15631	/note="vel1.1 pseudogene; similar to AAC78481.1 (PID:g3893863)"
	misc_feature	15452..16055	/note="similar to EST W38662 (NID:g1320367) zb98c07.r1"
	misc_feature	15552..16161	/note="similar to EST A1951839 (NID:g5744149) wx38c06.x1"
	misc_feature	15654..16163	/note="similar to EST AA411462 (NID:g2068994) zv30903.s1"
	misc_feature	15661..16158	/note="similar to EST AA148730 (NID:g1719241) zL44a10.s1"
	misc_feature	15682..16150	/note="similar to EST A1000399 (NID:g3190955) ct06f04.s1"
	misc_feature	15699..15690	/note="similar to EST W47207 (NID:g1331847) zc40g08.s1"
	misc_feature	15701..16166	/note="similar to EST AA076315 (NID:g1616245) zm91d05.s1"
	misc_feature	15715..16156	/note="similar to EST AA146982 (NID:g1716477) zo32f01.s1"
	misc_feature	15731..16148	/note="similar to EST H80236 (NID:g1058325) yu87e10.s1"
	misc_feature	15755..16158	/note="similar to EST AA969244 (NID:g3144424) on57b08.s1"
	misc_feature	15740..16160	/note="similar to EST W47207 (NID:g1331847) zc40g08.s1"
	misc_feature	15783..16159	/note="similar to EST AA948696 (NID:g3109949) oq49d05.s1"
	misc_feature	15860..16151	/note="similar to EST AA969829 (NID:g3145342) oc08h11.s1"
	misc_feature	15875..16151	/note="similar to EST A1675884 (NID:g4876364) wc06f07.x1"
	repeat_region	16162..16384	/rpt_family="L1"
	repeat_region	16395..16553	
	repeat_region		
	Query Match	3.5%; Score 46.6; DB 9; Length 107731;	
	Best Local Similarity	52.4%; Pred. No. 0.15;	
	Matches 100; Conservative	1; Mismatches 90; Indels 0; Gaps 0;	
OY	832 ATGTTACGCTTGAAGTAACGTATTCATTGTTGGTAAATAATTAATTAATGATACACGCC	891	
Db	3335 AAGTTACGATATAAAAAAGTACTCCTCCATCATATATGTAAGTTAATGACACGACT	3394	
OY	892 TACATTTGATCAATTTATTCGTCACACTGATTCCTCATCTTTAACGTAGAAGTGCG	951	
Db	3395 TTACACCAATTCATTTCTGCTGATCAACGACACGATCTCCAGATGAAATCTTGA	3454	
OY	952 AAAGCTAGGCACAAATTAACGGCTCTGCTGCGATTTACGATTTTACTGCAATTTTTTC	1011	
Db	3455 AAAGCCAAAGACTGACATTAATTTGATTTTGGATTTTCAATTAATTAATTAATTAATTA	3514	
OY	1012 CGATTGCCTTT	1022	
Db	3515 AACATCTCTTT	3525	

LOCUS AC048354 136551 bp DNA linear HNG 14-APR-2000
 DEFINITION Homo sapiens chromosome 16 clone CTC-345H14, LOW-PASS SEQUENCE
 SAMPLING.
 ACCESSION AC048354
 VERSION AC048354.1 GI:7549620
 KEYWORDS HTG: HTGS_PHASE0.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 136551)
 AUTHORS DOE Joint Genome Institute.
 TITLE Sequencing of Human Chromosome 16
 JOURNAL Unpublished
 2 (bases 1 to 136551)
 REFERENCE DOE Joint Genome Institute.
 AUTHORS Direct Submission
 TITLE Submitted (14-APR-2000) Production Sequencing Facility, DOE Joint
 JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 -----Genome Center
 Center: Joint Genome Institute
 Web site: <http://www.jgi.doe.gov>

* NOTE: This record contains 92 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

1 1019: contig of 1019 bp in length
 * 1020 1802: contig of 783 bp in length
 * 1803 2807: contig of 1005 bp in length
 * 2808 3822: contig of 1015 bp in length
 * 3823 5250: contig of 1428 bp in length
 * 5251 6271: contig of 1021 bp in length
 * 6272 7554: contig of 1283 bp in length
 * 7555 8338: contig of 784 bp in length
 * 8339 9477: contig of 1139 bp in length
 * 9478 10267: contig of 790 bp in length
 * 10268 11090: contig of 823 bp in length
 * 11091 12157: contig of 1067 bp in length
 * 12158 12967: contig of 810 bp in length
 * 12968 13772: contig of 805 bp in length
 * 13773 14990: contig of 1218 bp in length
 * 14991 15111: contig of 121 bp in length
 * 15112 16080: contig of 969 bp in length
 * 16081 16892: contig of 812 bp in length
 * 16893 17821: contig of 929 bp in length
 * gap of unknown length

* 17822 18526: contig of 705 bp in length
 * 18527 19587: contig of 1061 bp in length
 * 19588 20684: contig of 1097 bp in length
 * 20685 21449: contig of 765 bp in length
 * 21450 22430: contig of 981 bp in length
 * 22431 23323: contig of 893 bp in length
 * 23324 24068: contig of 745 bp in length
 * 24069 24828: contig of 760 bp in length
 * 24829 25757: contig of 929 bp in length
 * 25758 26813: contig of 1056 bp in length
 * 26814 27836: contig of 1023 bp in length
 * 27837 28912: contig of 1076 bp in length
 * 28913 29839: contig of 927 bp in length
 * 29840 30811: contig of 972 bp in length
 * 30812 31909: contig of 1098 bp in length
 * 31910 33295: contig of 1386 bp in length
 * 33296 34683: contig of 1388 bp in length
 * 34684 36215: contig of 1532 bp in length
 * 36216 37454: contig of 1239 bp in length
 * 37455 39106: contig of 1652 bp in length
 * 39107 40369: contig of 1263 bp in length
 * 40370 41799: contig of 1430 bp in length
 * 41800 43877: contig of 2078 bp in length
 * 43878 45004: contig of 1127 bp in length
 * 45005 46454: contig of 1450 bp in length
 * 46455 47458: contig of 1004 bp in length
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 * 48595 49351: contig of 757 bp in length
 * 49352 50486: contig of 1135 bp in length
 * 50487 51205: contig of 719 bp in length
 * 51206 52428: contig of 1223 bp in length
 * 52429 53679: contig of 1251 bp in length
 * 53680 54609: contig of 930 bp in length
 * 54610 55895: contig of 1286 bp in length
 * 55896 57444: contig of 1549 bp in length
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*	*	gap of unknown length
*	64333	65670: contig of 1338 bp in length
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*	65671	66708: contig of 1038 bp in length
*	*	gap of unknown length
*	66709	68120: contig of 1412 bp in length
*	*	gap of unknown length
*	68121	69823: contig of 1703 bp in length
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*	69824	71505: contig of 1682 bp in length
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*	71506	73111: contig of 1606 bp in length
*	*	gap of unknown length
*	73112	75036: contig of 1925 bp in length
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*	75037	76797: contig of 1761 bp in length
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*	76798	78157: contig of 1360 bp in length
*	*	gap of unknown length
*	78158	80268: contig of 2111 bp in length
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*	80269	81946: contig of 1678 bp in length
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*	81947	83710: contig of 1764 bp in length
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*	85616	86608: contig of 993 bp in length
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*	94137	95848: contig of 1712 bp in length
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*	95849	97468: contig of 1620 bp in length
*	*	gap of unknown length
*	97469	100052: contig of 2584 bp in length
*	*	gap of unknown length
*	100053	101688: contig of 1636 bp in length
*	*	gap of unknown length
*	101689	103434: contig of 1746 bp in length
*	*	gap of unknown length
*	103435	106504: contig of 3070 bp in length

Query Match

Best Local Similarity

Matches 137; Conservative

3.5%;

47.6%;

0;

Score 46.4;

Pred. No. 0; DB 2;

Mismatches 151; Indels 0;

Length 136551;

Gaps 0

Db 7235 TTTTCTTTTTCCTCCCTTTCTTTTTCCTAATGCCCTCTAATTATT 7176

Qy 1234 CGCGTACGCACTTTGATTTATTTTTCGAATGTTGTCGTAC 1281

Db 7175 TTTTCACTTTTATAATTTCCTCCCTCTTTTTCATCTGCC 7128

RESULT	12
AC097544/C	
LOCUS	229422 bp DNA linear HTG 12-JUL-2002
AC097544	
Rattus norvegicus clone CH4230-10207,	*** SEQUENCING IN PROGRESS
DEFINITION	*** /4 unordered pieces.

ACCESSION AC097544
VERSION AC097544.5 GI:21728623
KEYWORDS HTG: HNGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus

REFERENCE

1 (bases 1 to 229422)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., ...
... are I P Avele M. Banks,T.

AC097544 229422 bp DNA linear HTG-12-JUL-2002
Rattus norvegicus clone CH230-10207, *** SEQUENCING IN PROGRESS
***, 74 unordered pieces.
AC097544
AC097544.5 GI:21728623
HTG: HTGS_PHASE1.
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 3 (bases 1 to 229422)
AUTHORS Worley, K.C.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-2002) Human Genome Sequencing Center, Department

COMMENT

of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:17973416.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project name: GHMB

Center clone name: CH230-10207

Summary Statistics

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 158574 bases at least Q40

Consensus quality: 164750 bases at least Q30

Consensus quality: 169543 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
(see <http://www.hgsc.bcm.tmc.edu/docs/genbank.draft.data.html>).

NOTE: This is a 'working draft' sequence. It currently

consists of 74 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

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1 1077: contig of 1077 bp in length
* 1078 1177: gap of unknown length
* 1178 2279: contig of 1102 bp in length
* 2280 2379: gap of unknown length
* 2380 3440: contig of 1061 bp in length
* 3441 4654: gap of unknown length
* 4655 4755: gap of unknown length
* 4755 5839: contig of 1085 bp in length
* 5840 5939: gap of unknown length
* 5940 7595: contig of 1656 bp in length
* 7596 7696: gap of unknown length
* 7696 8853: contig of 1158 bp in length
* 8854 8954: gap of unknown length
* 8954 10166: contig of 1212 bp in length
* 10166 10266: gap of unknown length
* 10266 11745: contig of 1480 bp in length
* 11746 11845: gap of unknown length
* 11846 12848: contig of 1003 bp in length
* 12849 12948: gap of unknown length
* 12949 14505: contig of 1557 bp in length
* 14506 14605: gap of unknown length
* 14606 15923: contig of 1318 bp in length
* 15924 16023: gap of unknown length
* 16024 17271: contig of 1248 bp in length
* 17272 17371: gap of unknown length
* 17372 18474: contig of 1103 bp in length
* 18475 18574: gap of unknown length
* 18575 19720: contig of 1146 bp in length
* 19721 19820: gap of unknown length
* 19821 21097: contig of 1277 bp in length
* 21098 21197: gap of unknown length
* 21198 22523: contig of 1326 bp in length
* 22524 22623: gap of unknown length
* 22624 23810: contig of 1187 bp in length
* 23811 23910: gap of unknown length
* 23911 24943: contig of 1032 bp in length
* 24943 25042: gap of unknown length
* 25043 26566: contig of 1614 bp in length
* 26567 26757: gap of unknown length
* 26757 27846: contig of 1090 bp in length
* 27847 27947: gap of unknown length
* 27947 29722: contig of 1776 bp in length
* 29723 29822: gap of unknown length
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29823 31366: contig of 1544 bp in length
* 31367 31466: gap of unknown length
* 31467 33202: contig of 1736 bp in length
* 33203 33302: gap of unknown length
* 33303 34994: contig of 1692 bp in length
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* 35095 36771: contig of 1677 bp in length
* 36772 38806: contig of 1935 bp in length
* 38807 38907: gap of unknown length
* 38907 40645: contig of 1739 bp in length
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* 40746 42466: contig of 1721 bp in length
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* 44745 44844: gap of unknown length
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* 46936 47035: gap of unknown length
* 47036 49255: contig of 2220 bp in length
* 49256 49355: gap of unknown length
* 49356 50767: contig of 1412 bp in length
* 50768 52218: contig of 1351 bp in length
* 52219 52318: gap of unknown length
* 52319 53853: contig of 1535 bp in length
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* 53954 56201: contig of 2248 bp in length
* 56202 56301: gap of unknown length
* 56302 58728: contig of 2427 bp in length
* 58729 58829: gap of unknown length
* 58829 60272: contig of 1443 bp in length
* 60272 60372: gap of unknown length
* 60372 62519: contig of 2147 bp in length
* 62519 62619: gap of unknown length
* 62619 66044: contig of 3425 bp in length
* 66044 66144: gap of unknown length
* 66144 68947: contig of 2804 bp in length
* 68947 69047: gap of unknown length
* 69048 71619: contig of 2571 bp in length
* 71619 71719: gap of unknown length
* 71719 74043: contig of 2325 bp in length
* 74044 74144: gap of unknown length
* 74144 76323: contig of 2180 bp in length
* 76323 76423: gap of unknown length
* 76424 78433: contig of 2010 bp in length
* 78434 78533: gap of unknown length
* 78534 80017: contig of 1484 bp in length
* 80018 80117: gap of unknown length
* 80118 82845: contig of 2728 bp in length
* 82846 82945: gap of unknown length
* 82946 86645: contig of 3700 bp in length
* 86646 86745: gap of unknown length
* 86746 89688: contig of 2923 bp in length
* 89689 89788: gap of unknown length
* 89789 92784: contig of 3016 bp in length
* 92785 92884: gap of unknown length
* 92885 96529: contig of 3645 bp in length
* 96530 96630: gap of unknown length
* 96630 99447: contig of 2817 bp in length
* 99447 103361: contig of 3815 bp in length
* 103362 103461: gap of unknown length
* 103462 108371: contig of 4910 bp in length
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Query Match 3.5% Score 46; DB 2; Length 229422;

Best Local Similarity 43.18; Pred. No. 0.26;

Matches 88; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

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OY 1110 CGCGGTGGCCCTACGCTCCGCTTCTCCACATTTCCAAAGTACCGCTGATCTCATATA 1169
Db 1978 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
OY 1170 ATTCACTTCACTTAACTGCTCTTTTGTGTGGCTCTTCCAACTCCCAAAATTC 1229
```

[illegible]

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 242336)

Direct Submission
Submitted (11-Jul-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:17973592.

Genome Center

Center: Baylor College of Medicine

Center code: BCM
 Web site: <http://bcm.tmc.edu/>

Contact: hasc-hel@bcm.tmc.edu

----- Project Information

Center project name: GICX

Center clone name: CH230-192C3

Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye: 1000 01 1000
Assembly program: Phrap: version 0.990329

Consensus quality: 73499 bases at least Q40

Consensus quality: 78275 bases at least Q30

Consensus quality: 83602 bases at least Q20

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NOTE: Estimated insert size may differ from 5

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
 * NOPE: This is a "working draft" sequence. It currently
 * consists of 140 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1	1009: contig of 1009 bp in length
1010	gap of unknown length
1110	2236: contig of 1127 bp in length
2237	2336: gap of unknown length
2337	3388: contig of 1052 bp in length
3389	3488: gap of unknown length
3489	4660: contig of 1172 bp in length
4661	4760: gap of unknown length
4761	5777: contig of 1017 bp in length
5778	5877: gap of unknown length
5878	7036: contig of 1159 bp in length
7037	7136: gap of unknown length
7137	8162: contig of 1026 bp in length
8163	8852: gap of unknown length
8263	9364: contig of 1102 bp in length
9365	9464: gap of unknown length
9465	11357: contig of 1893 bp in length
11358	11457: gap of unknown length
11458	12535: contig of 1078 bp in length
12536	12635: gap of unknown length
12636	14100: contig of 1465 bp in length
14101	14200: gap of unknown length
14201	15554: contig of 1354 bp in length
15555	15654: gap of unknown length
15655	17062: contig of 1408 bp in length
17063	17162: gap of unknown length
17163	18321: contig of 1159 bp in length
18322	18421: gap of unknown length
18422	19642: contig of 1228 bp in length
19643	19749: gap of unknown length
19750	20936: contig of 1187 bp in length
20937	21036: gap of unknown length
21037	22163: contig of 1127 bp in length
22164	22263: gap of unknown length
22264	22397: contig of 1134 bp in length
22398	22497: gap of unknown length
23468	24532: contig of 1035 bp in length
24533	24632: gap of unknown length
24633	25783: contig of 1151 bp in length

QY	1167	ATAATTCATCTTACGATGTCGTCGTGGGCGCTTCACATCCCCCCAAAT	1266
Db	98441	ATAATATTTTTTTTTTTTTTTTGTTTTTTTTTTTTTTNNCCCCCCCCCCCC	98382
QY	1227	TTCGTGACGGGTACGGGACTTGATATATTTTTTTCACAATGTGTTCTCTACACAA	1266
Db	98381	CCNCCCNNGGCGTGTGGTGTTTTTTTTTTTTTTTTTATCTCCCTANAAAAA	98322
QY	1287	CAAAAAAAGCGTCAAAAAA 1315	
Db	98321	AAAAAAAAAAAAAAAAAAAAA 98293	

REFERENCE AUTHORS

REFERENCE

AUTHORS

1 (bases 1 to 170005)

Muzny,D.M., Adams,C., Adio-odunola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amarante,H.C., Are,J.R., Ayele,M., Banks,T., Barbarta,J., Benton,J., Blmage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Burch,C., Burch,P., Burkett,C., Butrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Deedrich,D.A., Delaney,K.R., Delgado,O., Penn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,D.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Hombl,F., Howard,S., Huber,J., Huyls,S., Hume,J., Jackson,L.E., Johnson,B., Jia,Y., Johnson,R., Jolyvet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratoch,C., Kurehli,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.I., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louisgeed,H., Lozada,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maestriwal,M., Mapua,P., Marlin,R., Martindale,A., Martinez,E., Massey,E., Mawlinney,E., Mcleod,M.P., Meador,M., Mel,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,M., Moser,M., Neal,D., Newton,J., Newton,K., Morgan,M., Morris,M., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Orangunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojudoakan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoochitari,N., Sisson,I., Sodergren,E., Sonalike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Umanal,K., Vasquez,L., Vera,Y., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S., Williams,G., Williamson,A., Wleciyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,Y., Zorrilla,S., Nelson,D., Weinstock,G., and Gibbs,R.

Eukaryota: Metazoa: Chordata: Cranialata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Rattus.

TITLE	Direct Submission
JOURNAL	unpublished
REFERENCE	2 (bases 1 to 170005)
AUTHORS	Worley, K.C.
TITLE	Direct Submission
JOURNAL	Submitted (12-JAN-2002)
	Human Genome Sequencing Center, Department

REFERENCE
AUTHORS
TITLE
JOURNAL

of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 170005)

COMMENT

Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced g1:18138812.

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GK01
Center clone name: CH230-72C9

----- Summary Statistics

Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 1008 of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 113946 bases at least Q40
Consensus quality: 121487 bases at least Q30
Consensus quality: 128156 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
(see <http://www.hgsc.bcm.tmc.edu/docs/genbank-draft-data.html>).

NOTE: This is a 'working draft' sequence. It currently
consists of 71 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

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1      1153: contig of 1153 bp in length
*      1154      1253: gap of unknown length
*      1254      2285: contig of 1032 bp in length
*      2286      2385: gap of unknown length
*      2386      3502: contig of 1117 bp in length
*      3503      3602: gap of unknown length
*      3603      5325: contig of 1723 bp in length
*      5326      5425: gap of unknown length
*      5426      6764: contig of 1339 bp in length
*      6765      6864: gap of unknown length
*      6865      7991: contig of 1127 bp in length
*      7992      8091: gap of unknown length
*      8092      9272: contig of 1181 bp in length
*      9273      9372: gap of unknown length
*      9373      10833: contig of 1461 bp in length
*      10834      10933: gap of unknown length
*      10934      12391: contig of 1458 bp in length
*      12392      12491: gap of unknown length
*      12492      13515: contig of 1024 bp in length
*      13516      13615: gap of unknown length
*      13616      15639: contig of 2024 bp in length
*      15640      15739: gap of unknown length
*      15740      16903: contig of 1164 bp in length
*      16904      17003: gap of unknown length
*      17004      18570: contig of 1567 bp in length
*      18571      18670: gap of unknown length
*      18672      19958: contig of 1288 bp in length
*      19959      20058: gap of unknown length
*      20059      21386: contig of 1328 bp in length
*      21387      21486: gap of unknown length
*      21487      22588: contig of 1102 bp in length
*      22589      22688: gap of unknown length
*      22689      23779: contig of 1091 bp in length
*      23780      23879: gap of unknown length
*      23880      25557: contig of 1678 bp in length
*      25558      25657: gap of unknown length
*      25658      27550: contig of 1893 bp in length
*      27551      27650: gap of unknown length

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*      27651      29682: contig of 2032 bp in length
*      29683      29782: gap of unknown length
*      29783      31436: contig of 1654 bp in length
*      31437      31536: gap of unknown length
*      31537      32749: contig of 1213 bp in length
*      32750      32849: gap of unknown length
*      32850      34367: contig of 1518 bp in length
*      34368      34467: gap of unknown length
*      34468      35540: contig of 1073 bp in length
*      35541      35640: gap of unknown length
*      35641      37378: contig of 1738 bp in length
*      37379      37478: gap of unknown length
*      37479      40174: contig of 2696 bp in length
*      40175      40274: gap of unknown length
*      40275      42050: contig of 1776 bp in length
*      42051      42150: gap of unknown length
*      42151      43567: contig of 1417 bp in length
*      43568      43667: gap of unknown length
*      43668      44712: contig of 1045 bp in length
*      44713      44812: gap of unknown length
*      44813      45993: contig of 1181 bp in length
*      45994      46093: gap of unknown length
*      46094      47679: contig of 1586 bp in length
*      47680      47779: gap of unknown length
*      47780      49052: contig of 1273 bp in length
*      49053      49152: gap of unknown length
*      49153      50987: contig of 1835 bp in length
*      50988      51087: gap of unknown length
*      51088      53149: contig of 2062 bp in length
*      53150      53249: gap of unknown length
*      53250      54528: contig of 1279 bp in length
*      54529      54628: gap of unknown length
*      54629      56210: contig of 1582 bp in length
*      56211      56310: gap of unknown length
*      56311      58009: contig of 1699 bp in length
*      58010      58109: gap of unknown length
*      58110      60268: contig of 2159 bp in length
*      60269      60368: gap of unknown length
*      60369      62307: contig of 1939 bp in length
*      62308      62407: gap of unknown length
*      62408      63892: contig of 1485 bp in length
*      63893      63992: gap of unknown length
*      63993      66676: contig of 2684 bp in length
*      66677      66776: gap of unknown length
*      66777      68795: contig of 2019 bp in length
*      68796      68895: gap of unknown length
*      68896      71185: contig of 2290 bp in length
*      71186      71285: gap of unknown length
*      71286      73230: contig of 1945 bp in length
*      73231      73330: gap of unknown length
*      73331      76851: contig of 3521 bp in length
*      76852      76951: gap of unknown length
*      76952      79277: contig of 2326 bp in length
*      79278      79377: gap of unknown length
*      79378      82280: contig of 2903 bp in length
*      82281      82380: gap of unknown length
*      82381      85008: contig of 2628 bp in length
*      85009      85108: gap of unknown length
*      85109      87508: contig of 2400 bp in length
*      87509      87608: gap of unknown length
*      87609      91272: contig of 3664 bp in length
*      91273      91372: gap of unknown length
*      91373      93438: contig of 2066 bp in length
*      93439      93538: gap of unknown length
*      93539      96282: contig of 2744 bp in length
*      96283      96382: gap of unknown length
*      96383      99441: contig of 3059 bp in length
*      99442      99541: gap of unknown length
*      99542      102218: contig of 2677 bp in length

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Query Match 3.58; Score 45.4; DB 2; Length 170005;
Best Local Similarity 48.6%; Pred. No. 0.36; Indels 0; Gaps 0;
Matches 118; Conservative 0; Mismatches 125;

289	3955:	contig of 1127 bp in length
3965	4055:	gap of unknown length
4056	5273:	contig of 1218 bp in length
5274	5373:	gap of unknown length
5374	6455:	contig of 1082 bp in length
6456	6555:	gap of unknown length
6556	7722:	contig of 1167 bp in length
7723	7822:	gap of unknown length
7823	8994:	contig of 1172 bp in length
8995	9094:	gap of unknown length
9095	10258:	contig of 1164 bp in length
10259	10358:	gap of unknown length
10359	11529:	contig of 1171 bp in length
11530	11629:	gap of unknown length
11630	12772:	contig of 1143 bp in length
12773	12872:	gap of unknown length
12873	13954:	contig of 1082 bp in length
13955	14054:	gap of unknown length
14055	15127:	contig of 1073 bp in length
15128	15227:	gap of unknown length
15228	16411:	contig of 1184 bp in length
15229	16511:	gap of unknown length
16512	17557:	contig of 1046 bp in length
17558	17657:	gap of unknown length
17658	18766:	contig of 1109 bp in length
18767	18866:	gap of unknown length
18867	20034:	contig of 1168 bp in length
20035	20134:	gap of unknown length
20135	21336:	contig of 1202 bp in length
21337	21436:	gap of unknown length
21437	22545:	contig of 1109 bp in length
22546	22645:	gap of unknown length
22646	23755:	contig of 1110 bp in length
23756	23855:	gap of unknown length
23856	24927:	contig of 1072 bp in length
24928	25027:	gap of unknown length
25028	26153:	contig of 1126 bp in length
26154	26253:	gap of unknown length
26254	27455:	contig of 1202 bp in length
27456	27555:	gap of unknown length
27556	28679:	contig of 1124 bp in length
28680	28779:	gap of unknown length
28780	29893:	contig of 1114 bp in length
29894	29994:	gap of unknown length
29994	31172:	contig of 1179 bp in length
31173	31273:	gap of unknown length
31273	32388:	contig of 1116 bp in length
32389	32488:	gap of unknown length
32489	33650:	contig of 1162 bp in length
33651	33750:	gap of unknown length
33751	34987:	contig of 1237 bp in length
34988	35087:	gap of unknown length
35088	36153:	contig of 1066 bp in length
36154	36253:	gap of unknown length
36254	37421:	contig of 1168 bp in length
37422	37521:	gap of unknown length
37522	38771:	contig of 1196 bp in length
38771	38817:	gap of unknown length
38818	39913:	contig of 1098 bp in length
39916	40015:	gap of unknown length
40016	41213:	contig of 1200 bp in length
41216	41315:	gap of unknown length
41316	42350:	contig of 1035 bp in length
42351	42450:	gap of unknown length
42451	43607:	contig of 1157 bp in length
43608	43707:	gap of unknown length
43708	44880:	contig of 1173 bp in length
44881	44980:	gap of unknown length
44981	46095:	contig of 1115 bp in length
46096	46195:	gap of unknown length
46196	47463:	contig of 1268 bp in length
47464	47563:	gap of unknown length
47564	48771:	contig of 1208 bp in length

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* 48772 48871: gap of unknown length
* 48872 50000: contig of 1129 bp in length
* 50001 50100: gap of unknown length
* 50101 51241: contig of 1141 bp in length
* 51242 51341: gap of unknown length
* 51342 52439: contig of 1098 bp in length
* 52440 52539: gap of unknown length
* 52540 53719: contig of 1180 bp in length
* 53720 53819: gap of unknown length
* 53820 54972: contig of 1153 bp in length
* 54973 55072: gap of unknown length
* 55073 56256: contig of 1184 bp in length
* 56257 56356: gap of unknown length
* 56357 57447: contig of 1091 bp in length
* 57448 57547: gap of unknown length
* 57548 58710: contig of 1163 bp in length
* 58711 58810: gap of unknown length
* 58811 59999: contig of 1189 bp in length
* 60000 60099: gap of unknown length
* 60100 61343: contig of 1244 bp in length
* 61344 61443: gap of unknown length
* 61444 62568: contig of 1125 bp in length
* 62569 62668: gap of unknown length
* 62669 63904: contig of 1236 bp in length
* 63905 64004: gap of unknown length
* 64005 65045: contig of 1041 bp in length
* 65046 65145: gap of unknown length
* 65146 66360: contig of 1215 bp in length
* 66361 66460: gap of unknown length
* 66461 67705: contig of 1245 bp in length
* 67706 67805: gap of unknown length
* 67806 68914: contig of 1109 bp in length
* 68915 69014: gap of unknown length
* 69015 70199: contig of 1185 bp in length
* 70200 70299: gap of unknown length
* 70300 71355: contig of 1056 bp in length
* 71356 71455: gap of unknown length
* 71456 73215: contig of 1760 bp in length
* 73216 73315: gap of unknown length
* 73316 74456: contig of 1141 bp in length
* 74457 74556: gap of unknown length
* 74557 76312: contig of 1756 bp in length
* 76313 76412: gap of unknown length
* 76413 77484: contig of 1072 bp in length
* 77485 77584: gap of unknown length
* 77585 78683: contig of 1099 bp in length
* 78684 78783: gap of unknown length
* 78784 79858: contig of 1075 bp in length
* 79859 79958: gap of unknown length
* 79959 80987: contig of 1029 bp in length
* 80988 81087: gap of unknown length
* 81088 82188: contig of 1101 bp in length
* 82189 82288: gap of unknown length
* 82289 83320: contig of 1032 bp in length
* 83321 83420: gap of unknown length
* 83421 84521: contig of 1101 bp in length
* 84522 84621: gap of unknown length
* 84622 101509: contig of 16888 bp in length.

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FEATURES
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 1. 101509
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="RP11-167D21"
 /clone_lib="RPCI human BAC library 11"

BASE COUNT 27989 a 7533 c 28794 g 7012 t 30181 others
 ORIGIN

Query Match 3.4%; Score 45.2; DB 2: Length 101509;
 Best Local Similarity 40.4%; Pred. No. 0.38;
 Matches 116; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

OY 987 TTACGATTCTACGCAATTTTTCGATTGCTTTTTCGCGCAACCTACTTCG 1046

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Db 3790 TTTCCCTTTTTCCTCCCTTTTCCTTTTCCCTTTTNNCCCTTCCTCCCTTTTCT 3731
OY 1047 CGTAATATCACTTTTCCGCTGCTGTACATTCGCAAAACCCGAAACCTACTTT 1106
Db 3730 TTTTTCCTCCCTTTTNNCTTTTCCCTTTTCCCTTTTCCCTTTTCCCTTTTCT 3671
OY 1107 TCTCCGCGTGCGCTAGCCCTCCCTCTCTCCACATTTCCAAAGTACCCGTATCTCA 1166
Db 3670 TTTNNNNNTTNNNNNNCCCTTTTNNCTTTTCCCTTTTCCCTTTTCCCTTTTCT 3611
OY 1167 ATAAATCATCTCACTTTTAACTGTCTCTTTGCTGTGCGCTTTCCACTCCGCCAAT 1226
Db 3610 TTTCCCTTTTTCCTTTTCCCTTTTCCCTTTTCCCTTTTCCCTTTTCCCTTTTCT 3551
OY 1227 TCCGTACGCTACGCGACCTGTGATTTATTTTTCATTTGTTTT 1273
Db 3550 TTTCTTNNCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3504

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Search completed: February 28, 2003, 03:32:43
 Job time : 4345.62 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 18:35:25 ; Search time 237.618 Seconds
(without alignments)
12462.745 Million cell updates/sec

Title: US-09-993-420A-2

Perfect score: 1315

Sequence: 1 tttagatgacacgctgcac.....cggttcaaaaaaaaaaaaaa 1315

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
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9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
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18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
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21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1311.4	99.7	1315 15	AA054630
2	632.6	48.1	15	AA054629
3	44.2	3.4	23	ABY60941
4	41.4	3.2	22	AA158066
5	41.4	3.1	24	AB052458
6	41.4	3.1	24	AB052459
7	40.2	3.1	22	AA188595
8	39.8	3.0	22	AA182664
9	39.8	3.0	22	AA060450

C 10	39.8	3.0	425	22	AA060450	Human cancer agent
C 11	39.6	3.0	458	24	AB193709	Arabidopsis thaliana
C 12	39.6	3.0	556	23	ABY40063	Human prostate exp
C 13	39.6	3.0	536	23	ABY40163	Human prostate exp
C 14	39.6	3.0	556	23	ABY42105	Human prostate exp
C 15	39.6	3.0	556	23	ABY43601	Human prostate exp
C 16	39.6	3.0	612	22	AAH71471	Human cervical can
C 17	39.6	3.0	2970	20	AA020290	Borrelia burgdorferi
C 18	39.4	3.0	426	23	ABY60871	Human prostate exp
C 19	39.4	3.0	1315	21	AA05464	Human secreted pro
C 20	39.4	3.0	1680	21	AA098827	Human secreted pro
C 21	39.4	3.0	8789	23	AB103040	Drosophila melanog
C 22	38.8	2.9	9507	24	ABN80242	Human chemically m
C 23	38.6	2.9	299	23	ABY61374	Human prostate exp
C 24	38.6	2.9	408	22	AA193518	Human polynucleoti
C 25	38.4	2.9	405	22	AA065332	Novel human polyn
C 26	38.4	2.9	8323	24	AB132058	Human immune syste
C 27	38.2	2.9	6222	24	AB132692	Human immune syste
C 28	38	2.9	556	23	ABY40063	Human prostate exp
C 29	38	2.9	556	23	ABY40163	Human prostate exp
C 30	38	2.9	556	23	ABY42105	Human prostate exp
C 31	38	2.9	556	23	ABY43601	Human prostate exp
C 32	38	2.9	608	24	AB066317	Human prostate exp
C 33	38	2.9	1542	21	AAA10594	Arabidopsis thaliana
C 34	38	2.9	10732	21	AAA10594	DNA encoding a hum
C 35	38	2.9	17848	22	AA054532	Chemically pretrea
C 36	38	2.9	17848	22	ABK39875	Human chemically p
C 37	38	2.9	17848	24	ABK28163	Human transcription
C 38	37.8	2.9	417	21	AA024643	Human secreted pro
C 39	37.8	2.9	3492	23	AA066669	Drosophila melanog
C 40	37.8	2.9	7261	22	AA066669	Tumour suppressor
C 41	37.6	2.9	5432	24	ABN80000	Human chemically m
C 42	37.6	2.9	6031	22	AA054621	Tumour suppressor
C 43	37.4	2.8	278	22	AAH69999	Human cervical can
C 44	37.4	2.8	4590	22	AAH24065	Human secreted pro
C 45	37.4	2.8	6229	24	AB132264	Human immune syste

ALIGNMENTS

RESULT 1
AA054630
ID AA054630 standard; cDNA to mRNA; 1315 BP.

XX AA054630;

XX 23-JUN-1994 (first entry)

XX ced-9 coding sequence.

XX ced-9 coding sequence.

KW Cell death; senescence; programmed cell death; ced-9; myocardial

KW Infarction; stroke; brain injury; neurodegenerative disease;

KW muscular degenerative disease; ageing; hypoxia; ischaemia; toxemia;

KW infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2;

KW oncogene; ss.

XX Caenorhabditis elegans.

XX W09325683-A.

XX 23-DEC-1993.

XX 14-JUN-1993; 93WO-US05651.

XX 12-JUN-1992; 92US-0898933.

XX 10-AUG-1992; 92US-0927681.

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX Hengartner M, Horvitz HR;
 PI WPI: 1994-007540/01.
 DR P-PSDB: AAR47343.
 XX Caenorhabditis elegans cell death-protective gene - used to
 PT prevent agents for preventing cell death or for reducing
 PT population of cells
 PS Claim 3: Page 58-59; 112pp: English.
 XX Ccd-9 is essential for C. elegans development and apparently
 CC functions by protecting cells during development from programmed
 CC cell death. Ccd-9 was shown to function by antagonising the
 CC activities of cell death genes ced-3 and ced-4. The protein product
 CC of the human oncogene bcl-2 was found to have a similar sequence
 CC to the ced-9 protein. The ced-9 gene can be used for developing
 CC agents for treating a condition characterised by increased cell death
 CC such as myocardial infarction, stroke, traumatic brain injury,
 CC neurodegenerative disease, muscular degenerative disease, ageing,
 CC hypoxia, ischaemia, toxemia, infection or hair loss. It can also
 CC be used for reducing a population of cells in the treatment of
 CC neoplastic growth cancerous tissue, infected cells or autoreactive
 CC immune cells.
 XX SQ Sequence 1315 BP; 362 A; 290 C; 315 G; 347 T; 1 other:
 Query Match 99.7%; Score 1311.4; DB 15; Length 1315;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 601 TTGCTTACACATCGCTGTTTCATCAAAACGCGATCCGCAACACTGAGAGACACAT 660
 |||||||
 Db 601 TTGCTTACACATCGCTGTTTCATCAAAACGCGATCCGCAACACTGAGAGACACAT 660
 QY 661 CGAGCTGGAGACACTTTCATGCACTCGGAAAAAACAATGAAAGAGACTACGACGACA 720
 |||||||
 Db 661 CGAGCTGGAGACACTTTCATGCACTCGGAAAAAACAATGAAAGAGACTACGACGACA 720
 QY 721 GAAGCTGAAAAAGTGGGAGCGCGGAAAGCAAGACAGCGGTGTCGATTTGGCCCTGGA 780
 |||||||
 Db 721 GAAGCTGAAAAAGTGGGAGCGCGGAAAGCAAGACAGCGGTGTCGATTTGGCCCTGGA 780
 QY 781 GTACAGCTGAGACATTTGGAATCGTTGAGTCGTCGTGTGTGGCGGATGATGTTCAAGC 840
 |||||||
 Db 781 GTACAGCTGAGACATTTGGAATCGTTGAGTCGTCGTGTGTGGCGGATGATGTTCAAGC 840
 QY 841 TTGACGTACGATTTTAAATTTGTTGTAATTAATTTATGTAACACTCTTACATTTGA 900
 |||||||
 Db 841 TTGACGTACGATTTTAAATTTGTTGTAATTAATTTATGTAACACTCTTACATTTGA 900
 QY 901 ATCTCAATTTKGTCTCACTGATTTCTCATCTTTGAACTGGAAGAGTGGAAAGCTAGG 960
 |||||||
 Db 901 ATCTCAATTTKGTCTCACTGATTTCTCATCTTTGAACTGGAAGAGTGGAAAGCTAGG 960
 QY 961 CCACAAATTTACGGCTCTGTGTGATTTAGCAATTTTACTGCAATTTTTCGATTTGCT 1020
 |||||||
 Db 961 CCACAAATTTACGGCTCTGTGTGATTTAGCAATTTTACTGCAATTTTTCGATTTGCT 1020
 QY 1021 TTTTGTGTCGCAAAACCTTACTTCCGCTATATCACTTTCCGTTCTGTACATTTTC 1080
 |||||||
 Db 1021 TTTTGTGTCGCAAAACCTTACTTCCGCTATATCACTTTCCGTTCTGTACATTTTC 1080
 QY 1081 GTCAAAAACCTGAAACCTTACTTTCGCGGTGAGCTCCGCTTCTCTTCA 1140
 |||||||
 Db 1081 GTCAAAAACCTGAAACCTTACTTTCGCGGTGAGCTCCGCTTCTCTTCA 1140
 QY 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTCATCTTCACTTTTCTCTTCTGT 1200
 |||||||
 Db 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTCATCTTCACTTTTCTCTTCTGT 1200
 QY 1201 GTGGCCCTTCCAAATCCCCCAATTCCTGTACGGGTACGGGACTTTGATTTATTTT 1260
 |||||||
 Db 1201 GTGGCCCTTCCAAATCCCCCAATTCCTGTACGGGTACGGGACTTTGATTTATTTT 1260
 QY 1261 TTCAATTTGTTTCTCTCTCAACAACAAAAAAGGTTTCAAAAAA 1315
 |||||||
 Db 1261 TTCAATTTGTTTCTCTCTCAACAACAAAAAAGGTTTCAAAAAA 1315

RESULT 2
 AA054629
 ID AA054629 standard; DNA; 6560 BP.
 XX AC AA054629;
 XX AC
 XX 23-JUN-1994 (first entry)
 XX DE
 XX Genomic region containing ced-9 gene.
 XX KW
 KW Cell death; senescence; programmed cell death; ced-9; myocardial
 KW infarction; stroke; brain injury; neurodegenerative disease;
 KW muscular degenerative disease; ageing; hypoxia; ischaemia; toxemia;
 KW infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2;
 KW oncogene; ss.
 XX OS
 OS Caenorhabditis elegans.
 XX PN
 PN W09325683-A.
 XX PD
 PD 23-DEC-1993.
 XX PF
 PF 14-JUN-1993; 93WO-US05651.

Query	1209	TTGCAATCCCCCAAAATTCCTGTAACGCGTAACGCACTTTGTATTATTTTTCCTCAATT	1268
Db	3873	AAAGTACCGCGTATGTCATTAATTAATCACTCTTAACTGTCGTCTGTCGTCGTC	3932
Qy	1149	AAATGACCCCTGATATTCATTAATATCATCTTAACTGTCGTCTGTCGTCGTC	1208
Db	3813	CCCTGGAACCCCTATCTTTCTCGCGGTGCGCTACGCTCCCGCTCTCTCCACATTTTCCA	3872
Qy	1089	CCCTGGAACCCCTATCTTTCTCGCGGTGCGCTACGCTCCCGCTCTCTCCACATTTTCCA	1148
Db	3693	TACGGCTCTCTGTGTGATTTACGATTTTACTGCAATTTTTCGGATTTGCTTTTTTTT	3752
Qy	969	TACGGCTCTCTGTGTGATTTACGATTTTACTGCAATTTTTCGGATTTGCTTTTTTTT	1028
Db	3633	TTTGCTACATGATTTCTCTATCTTGTGAACGTGAAGATGGGAACCTAGGCGCACAAAT	3692
Qy	909	TTTGCTACATGATTTCTCTATCTTGTGAACGTGAAGATGGGAACCTAGGCGCACAAAT	968
Db	3573	ACGATTTCAATTTGTGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	3532
Qy	849	ACGATTTCAATTTGTGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	908
Db	3513	TGGAGCCATTTGATGATGCTGTGTGTGGGGGATGATGATTCAGCTTGAAGTA	3572
Qy	789	TGGAGCCATTTGATGATGCTGTGTGTGGGGGATGATGATTCAGCTTGAAGTA	848
Db	3453	AAAAGTGGACGCGCGGAAACAGACAGACGCGTGCATGATTTGGCGCTGAGTAACAGC	788
Qy	729	AAAAGTGGACGCGCGGAAACAGACAGACGCGTGCATGATTTGGCGCTGAGTAACAGC	728
Db	3393	GGACGATTCATATACACTCTGGAAAAAATGAAGAGACACAGACAGACAGCTGA	3452
Qy	669	GGACGATTCATATACACTCTGGAAAAAATGAAGAGACACAGACAGACAGCTGA	728
Query Match	48.1%	Score 632.6;	DB 15; Length 6560;
Best Local Similarity	99.8%	Pred. No. 4.8e-172;	
Matches 632;	Conservative 1;	Mismatches 0;	Indels 0; Gaps 0;

Dd		3993	TTCGACATCCCCCAAAATCTCGTACGGGTACGCAGCATTTGAATTATTTTTCCAAAT	3992
Oy	1269	GTTTTCCTCTCACAACAACAAAAAAGCGTTC	1301	
Dd	3993	GTTTCTCTCTACACAACAACAAAAAACGGTTC	4025	
RESULT 3				
ABV60941/c				
ID	ABV60941	standard;	CDNA; 626 BP.	
XX				
AC				
XX	ABV60941;			
XX				
DE	13-SEP-2002	(first entry)		
XX				
DE		Human prostate expression marker CDNA 60932.		
XX				
KW		Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;		
RW		pharmacogenomic marker; gene; ss.		
XX				
OS	Homo sapiens.			
XX				
PX	WO200160860-A2.			
PN				
PD	23-AUG-2001.			
PF				
XX	20-FEB-2001; 2001WO-US05171.			
PR	17-FEB-2000; 2000US-183319P.			
PR	16-MAR-2000; 2000US-189862P.			
PR	25-MAY-2000; 2000US-207454P.			
PR	09-JUN-2000; 2000US-21314P.			
PR	18-JUL-2000; 2000US-219007P.			
PR	13-DEC-2000; 2000US-255281P.			
PA				
(MILL.)	MILLENNIUM PREDICTIVE MEDICINE INC.			
PI	Schlegel R, Endege WO, Monahan JE;			
DR	WPI; 2001-662795/76.			
PT				
Novel	isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -			
PS	Claim 1; Page 11585; 11750bp; English.			
The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:				
(a) assessing whether a patient is afflicted with prostate cancer;				
(b) monitoring the progression of prostate cancer in a patient;				
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;				
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;				
(e) selecting a composition for inhibiting prostate cancer in a patient;				
(f) assessing the prostate cell carcinogenic potential of a compound;				
(g) determining whether prostate cancer has metastasized in a patient;				
(h) assessing the aggressiveness or indolence of prostate cancer in a patient;				
(I) is also useful as a pharmacodynamic or pharmacogenomic marker.				
Sequence 626 BP; 356 A; 15 C; 41 G; 130 T; 84 other;				
Query Match	3.4%;	Score 44.2;	DB 23;	Length 626;
Best Local Similarity	40.8%;	Pred. No. 0.023;		
Matches 139;	Conservative 0;	Mismatches 202;	Indels 0;	Gaps 0;
OY	975 TCCTGCTGTCGACATTTTCGAAATTTTCCGATTCGCCCTTTTGTGGCAA	1034		
I	I I I I			
Dd	438 TATTTTNTNTTTTAATTTTITTTTANGCCNGNNGNCITTTTNTTTTITTATNTTN	379		


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OS      Homo sapiens.
XX
PN      WO200179556-A2.
XX
PD      25-Oct-2001.
XX
PF      13-Apr-2001; 2001WO-US12132.
XX
PR      14-Apr-2000; 2000US-197538P.
XX
PA      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI      Lillie J, Brown JL, Bolt A, Van Huffel C;
XX
DR      WPI; 2001-602933/68.
XX
PT      Novel nucleic acid, used as a marker to determine the effectiveness of
PS      using TAXOL to treat cancer cell growth in individuals -
XX
PS      Claim 1; Page 221; 527pp; English.
XX
CC      The invention relates to 1046 novel nucleic acids which are used as
CC      markers for determining the sensitivity of a cancer cell to the
CC      anticancer agent TAXOL. Cancer cells can be treated with TAXOL when
CC      they are shown to express one of the 242 sensitivity markers or the
CC      cells are shown not to express one of the 804 resistance markers.
CC      The methods can be used to determine the effectiveness of TAXOL
CC      in the treatment of cancer cell growth in an individual. The markers
CC      can be used as targets in developing anti-cancer agents such as
CC      chemotherapeutic compounds. The markers can also be used as targets in
CC      developing treatments for cancer, particularly those cancers which
CC      anticancer agents developed by the novel method can be used to treat
CC      cancer. Probes based on the markers can be used to detect transcripts or
CC      genomic sequences corresponding to the markers, in the identification of
CC      cells or tissues which mis-express the protein. Cancers which may
CC      be targeted include carcinoma (e.g. squamous cell carcinoma),
CC      sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia),
CC      lymphoma, plasmacytoma, reticulum cell sarcoma, Hodgkin's disease and
CC      tumours (e.g. glioma). The present sequence is one of the 1046
CC      novel cancer cell markers.
XX
SQ      Sequence 425 BP; 159 A; 41 C; 28 G; 194 T; 3 other;
XX
Query Match          3.0%; Score 39.8; DB 22; Length 425;
Best Local Similarity 71.4%; Pred. No. 0.36;
Matches 50; Conservative 0; Mismatches 20; Indels 0; Gaps 0
QY      1246 TTGTATTATTTATTTTCAATGTTCTTCACACAAACAAAGGTTCAA 1305
DB      76 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 135
OY      1306 AAAAAAAAAA 1315
DDB     136 AAAAAAAAAA 145
RESULT 10
AAS60450/c
ID      AAS60450 standard; cDNA; 425 BP.
XX
XX      AAS60450;
XX
DT      29-JAN-2002 (first entry)
DE      Human cancer agent-sensitive marker #181.
XX
KW      Human; cancer cell marker; TAXOL; cytostatic; tumour; Carcinoma;
KW      squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
KW      lymphocytic leukaemia; lymphoma; plasmacytoma; reticulum cell sarcoma;
KW      Hodgkin's disease; glioma; ss.
XX
SS      Homo sapiens.

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XX XX
PN PN      MO200179556-A2.
XX XX
PD PD      25-OCT-2001.
XX XX
PF PF      13-APR-2001; 2001WO-US12132.
XX XX
PR PR      14-APR-2000; 2000US-197538P.
XX XX
PA PA      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX XX
PI PI      Little J, Brown JL, Bolt A, Van Hufel C;
XX XX
DR DR      WPI: 2001-602933/68.
XX XX
PT PT      Novel nucleic acid, used as a marker to determine the effectiveness of
PT PT      using TAXOL to treat cancer cell growth in individuals -
XX XX
PS PS      Claim 1; Page 221; 527pp; English.

The invention relates to 1046 novel nucleic acids which are used as
CC markers for determining the sensitivity of a cancer cell to the
CC anticancer agent TAXOL. Cancer cells can be treated with TAXOL when
CC they are shown to express one of the 242 sensitivity markers or the
CC cells are shown not to express one of the 804 resistance markers.
CC The methods can be used to determine the effectiveness of TAXOL.
CC in the treatment of cancer cell growth in an individual. The markers
CC can be used as targets in developing anti-cancer agents such as
CC chemotherapeutic compounds. The markers can also be used as targets in
CC developing treatments for cancer, particularly those cancers which
CC displaying resistance to agents and exhibit expression of the markers. The
CC anticancer agents developed by the novel method can be used to treat
CC cancer. Probes based on the markers can be used to detect transcripts or
CC genomic sequences corresponding to the markers, in the identification of
CC cells or tissues which mis-express the proteins. Cancers which may
CC be targeted include carcinoma (e.g., squamous cell carcinoma),
CC sarcoma (e.g., fibrosarcoma) leukaemia (e.g., lymphocytic leukaemia),
CC lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's disease and
CC tumours (e.g., glioma). The present sequence is one of the 1046
CC novel cancer cell markers.
XX XX
SQ SQ      Sequence 425 BP; 159 A; 41 C; 28 G; 194 T; 3 other;

Query Match
Best Local Similarity 3.0%; Score 39.8; DB 22; Length 425;
Matches 50; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1246 TTGTGATTTATTTTTCATATGTTTCTCTACACACACAAAAACGGTTCAAAA 1305
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 147 TTTTTTTTTTTTTTTTAAATTTTTTTTTTTTTTTNNNAAAAA
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1306 AAAAAA 1315
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 87 AAAAAA 78

RESULT 11
ABL93709/c
ID ABL93709 standard; cDNA; 458 BP.
XX AC
XX ABL93709;
XX DT
XX 10-JUN-2002 (first entry)
XX DE
XX Arabidopsis thaliana nucleic acid sequence Ref:2027474 SEQ ID NO:474.
XX DE
XX Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis;
XX genetic modification; gene; ss.
XX KW
XX Arabidopsis thaliana.
XX OS
XX Arabidopsis thaliana.
XX NN
US2002023280-A1.

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GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 19:36:05 ; Search time 40.2432 Seconds

(without alignments)
10021.077 Million cell updates/sec

Title: US-09-993-420A-2

Perfect score: 1315
Sequence: 1 ttgagatgacacgctgcac.....cgttcaaaaaaaaaaaaaa 1315

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA:*

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6: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1314.6	100.0	1315	US-09-234-186-2	Sequence 2, Appl
2	1314.6	100.0	1315	US-09-233-527-2	Sequence 2, Appl
3	1314.6	100.0	1315	PCT-US93-05651-2	Sequence 2, Appl
4	1313	99.8	1315	US-09-234-186-4	Sequence 4, Appl
5	1313	99.8	1315	US-09-234-186-5	Sequence 5, Appl
6	1313	99.8	1315	US-09-234-186-6	Sequence 6, Appl
7	1313	99.8	1315	US-09-233-527-4	Sequence 4, Appl
8	1313	99.8	1315	US-09-233-527-5	Sequence 5, Appl
9	1313	99.8	1315	US-09-233-527-6	Sequence 6, Appl
10	632.6	48.1	6559	US-09-234-186-1	Sequence 1, Appl
11	632.6	48.1	6559	US-09-233-527-1	Sequence 1, Appl
12	632.6	48.1	6560	PCT-US93-05651-1	Sequence 1, Appl
13	81.8	6.2	7218	US-08-232-463-14	Sequence 14, Appl
14	55.6	4.2	7218	US-08-232-463-14	Sequence 14, Appl
15	47.6	3.6	289	US-09-007-005-17	Sequence 17, Appl
16	47.6	3.6	289	US-09-244-796-17	Sequence 17, Appl
17	36.8	2.8	2395	US-09-244-796-17	Sequence 17, Appl
18	36.8	2.8	1299	US-09-149-476-159	Sequence 159, Appl
19	36.4	2.8	5852	US-09-222-938A-39	Sequence 39, Appl
20	35.6	2.7	289	US-07-867-106-2	Sequence 2, Appl
21	35.6	2.7	289	US-09-007-005-17	Sequence 17, Appl
22	35.4	2.7	1307	US-09-244-796-17	Sequence 17, Appl
23	35	2.7	248	US-09-007-005-32	Sequence 32, Appl
24	35	2.7	248	US-09-244-796-32	Sequence 32, Appl
25	35	2.7	277	US-09-007-005-3	Sequence 3, Appl
26	35	2.7	277	US-09-244-796-3	Sequence 3, Appl
27	34.8	2.6	1033	US-09-173-300-46	Sequence 46, Appl

28	34.8	2.6	3073	1	US-07-688-352C-31	Sequence 31, Appl
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37	33.4	2.5	1096	4	US-09-461-697-26	Sequence 26, Appl
38	33.4	2.5	2791	4	US-09-570-367C-1	Sequence 1, Appl
39	33.2	2.5	1313	4	US-09-149-476-112	Sequence 112, App
40	33.2	2.5	2007	3	US-08-747-221B-38	Sequence 38, Appl
41	33.2	2.5	2007	3	US-08-747-221B-38	Sequence 38, Appl
42	33.2	2.5	2007	4	US-09-005-051-36	Sequence 36, Appl
43	33.2	2.5	2007	4	US-09-005-051-36	Sequence 38, Appl
44	33	2.5	1466	4	US-08-984-919A-10	Sequence 10, Appl
45	33	2.5	1466	4	US-08-984-919A-12	Sequence 12, Appl

ALIGNMENTS

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RESULT 1
US-09-234-186-2
: Sequence 2, Application US/09234186
: Patent No. 6312947
: GENERAL INFORMATION:
: APPLICANT: Horvitz, H. Robert
: APPLICANT: Hengartner, Michael
: TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
: TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: 01997/201005
: CURRENT APPLICATION NUMBER: US/09/234,186
: CURRENT FILING DATE: 1999-01-20
: EARLIER APPLICATION NUMBER: 07/898,933
: EARLIER FILING DATE: 1992-06-12
: EARLIER APPLICATION NUMBER: 07/927,681
: EARLIER FILING DATE: 1992-08-10
: EARLIER APPLICATION NUMBER: 08/288,295
: EARLIER FILING DATE: 1994-08-10
: EARLIER APPLICATION NUMBER: 08/801,248
: EARLIER FILING DATE: 1997-02-19
: NUMBER OF SEQ. ID NOS.: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 1315
: TYPE: DNA
: ORGANISM: Caenorhabditis elegans
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (7)...(846)
US-09-234-186-2

Query Match      100.0%   Score 1314.6;   DB 4;   Length 1315;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 1315;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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RESULT 2
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 ; Sequence 2, Application US/09233527
 ; Patent No. 6465617
 ; GENERAL INFORMATION:
 ; APPLICANT: Horvitz, H. Robert
 ; APPLICANT: Hengartner, Michael
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 ; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
 ; FILE REFERENCE: 0197/201004
 ; CURRENT FILING DATE: 1999-01-20
 ; PRIOR FILING DATE: 1997-02-19
 ; PRIOR FILING DATE: 1992-06-12
 ; PRIOR FILING DATE: 1992-08-10
 ; PRIOR FILING DATE: 1992-08-10
 ; PRIOR FILING DATE: 1994-08-10
 ; PRIOR FILING DATE: 1997-02-19
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1315
 ; TYPE: DNA
 ; ORGANISM: Caenorhabditis elegans
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (7)...(846)
 US-09-233-527-2
 Query Match 100.0%; Score 1314.6; DB 4; Length 1315;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
US-09-234-186-4
: Sequence 4, Application US/09234186
: Patent No. 6312947
: GENERAL INFORMATION:
: APPLICANT: Horvitz, H. Robert
: APPLICANT: Hengartner, Michael
: TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
: TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: 01997/201005
: CURRENT APPLICATION NUMBER: US/09/234,186
: EARLIER FILING DATE: 1999-01-20
: EARLIER APPLICATION NUMBER: 07/898,933
: EARLIER FILING DATE: 1992-06-12
: EARLIER APPLICATION NUMBER: 07/927,681
: EARLIER FILING DATE: 1992-08-10
: EARLIER APPLICATION NUMBER: 08/288,295
: EARLIER FILING DATE: 1994-08-10
: EARLIER APPLICATION NUMBER: 08/801,248
: EARLIER FILING DATE: 1997-02-19
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 1315
: TYPE: DNA
: ORGANISM: Caenorhabditis elegans
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (7)...(846)
US-09-234-186-4

Query Match 99.8%; Score 1313; DB 4; Length 1315;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1261 TTCAAATGTTTCTCTCTACACACACAAAAAAGGTTCAAAAAA 1315

RESULT 5
US-09-234-186-5 Application US/09234186

; Sequence 5, Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; CURRENT FILING DATE: 1999-01-20
; EARLIER FILING DATE: 07/898,933
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-234-186-5

Query Match 99.8%; Score 1313; DB 4; Length 1315;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1201 GTGGCCTTTCGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 TTCAAATTTGTTTCTCTCTCTACACACAAAAAAGGTTCAAAAAA 1315
Db 1261 TTCAAATTTGTTTCTCTCTCTACACACAAAAAAGGTTCAAAAAA 1315

RESULT 6
US-09-234-186-6
; Sequence 6, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; CURRENT FILING DATE: 1999-01-20
; EARLIER FILING DATE: 07/898,933
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 08/288,295

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; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-234-186-6

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Query Match          99.8%; Score 1313; DB 4; Length 1315;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 TTTGAGATGACACGCTGACGCGGACAACTCGTGACGAATCCGGCGTATCGGCGACGA 60
Db 1 TTTGAGATGACACGCTGACGCGGACAACTCGTGACGAATCCGGCGTATCGGCGACGA 60
QY 61 ACGATGGCGACTGCGGAGATGAGAGATTTCTGGGATMAAAGCACAGACCCACCGAT 120
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QY 121 TTTGAAATCAATAGTATGATGCTCAGACTTGGCATCAGGAGTAGGCGAGGCTTCGACGGGA 180
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Db 181 AGAATGTCATCGGAGCTCAATTTGATGAAAATCAATGATTTGGGAGAGCCAAAGGCTT 240
QY 241 GATATCGAGGAGTTGTGTGACTATTTACGACGACCGAATCCGGCAAAAGGAAATGGAA 300
Db 241 GATATCGAGGAGTTGTGTGACTATTTACGACGACCGAATCCGGCAAAAGGAAATGGAA 300
QY 301 TGGTTTGGAGCACCGGAGATTGCGGTGTGAGTGCACACCGGAGCAAGAAATGATCGAGTT 360
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QY 361 ATGGGAACGATTTTGGAAAGACAGACCGGAAATTTTGGACCTTGTGACGACCTG 420
Db 361 ATGGGAACGATTTTGGAAAGACAGACCGGAAATTTTGGACCTTGTGACGACCTG 420
QY 421 CTGCGAGTGCACGATCTCAATTTTCACTGATACGAGTGTGTTGGAGCGGTTGGAAT 480
Db 421 CTGCGAGTGCACGATCTCAATTTTCACTGATACGAGTGTGTTGGAGCGGTTGGAAT 480
QY 481 GCACAGACAGATCAATGTCCAATGCTTATGAGAGTGTGATAGTCTTAATCTGTTGCGC 540
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QY 541 GGTTCGTAGTGCAGAAAATATGAAATCCGTGAACTGCGAGGAGCAAGTCCGAAACCTC 600
Db 541 GGTTCGTAGTGCAGAAAATATGAAATCCGTGAACTGCGAGGAGCAAGTCCGAAACCTC 600
QY 601 TTGCTTTACACATGCTGTTTCATCAAAACGCGATCCGCAACACTGGAAGGAAACACAT 660
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Db 661 CGGAGCTGGGACGACTTCATGACACTCGGAAAACAAATGAAAGAGGACTACGAAAGGACA 720
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Db 721 GAAGCTGAAAAGTGGGAGCGCGGAGAGAGAACGAGCGTGTGATGATTTGGGCGTGGGA 780
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Db 841 TTGAGTAAGTAATTCATTTGTGTAATTAATTAATTTATGTAACAGCTTACATTGA 900
QY 901 ATCTCATTTTTCGCTACATGATCTCTCATCCCTTTGAAGTGAAGAGTGGAAAGCTAGG 960
Db 901 ATCTCATTTTTCGCTACATGATCTCTCATCCCTTTGAAGTGAAGAGTGGAAAGCTAGG 960
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QY 1081 GTCAAAAACCCCTGAACCCCTAATTTTCGCGGCTAGCCTCCGCTCTGTACCA 1140
Db 1081 GTCAAAAACCCCTGAACCCCTAATTTTCGCGGCTAGCCTCCGCTCTGTACCA 1140
QY 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTCATTTTAACTGCTCTTTTGGT 1200
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Db 1201 GTGGCCCTTTCGAACTCCCGCCCAATTCGTAAGCGGTACGCGGACTTTGATTTATTTT 1260
QY 1261 TTCAAAATGTTTCTCTCTACCAACAAACAAAAACGTTTCAAAAAA 1315
Db 1261 TTCAAAATGTTTCTCTCTACCAACAAACAAAAACGTTTCAAAAAA 1315

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RESULT 7
US-09-233-527-4
; Sequence 4, Application US/09233527
; Patent No. 6465617
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201004
; CURRENT APPLICATION NUMBER: US/09/233,527
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-233-527-4

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Query Match          99.8%; Score 1313; DB 4; Length 1315;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTTGAGATGACACGCTGACGCGGACAACTCGTGACGAATCCGGCGTATCGGCGACGA 60
Db 1 TTTGAGATGACACGCTGACGCGGACAACTCGTGACGAATCCGGCGTATCGGCGACGA 60

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QY 61 ACAGTGGGAGCTGGGAGATGAAGAGTTCCTGGGATTAAGAGCAGACAGCCACCGAT 120
 DB 61 ACAGTGGGAGCTGGGAGATGAAGAGTTCCTGGGATTAAGAGCAGACAGCCACCGAT 120
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 DB 121 TTGGAATCAATAGTAGTCTCAGAGACTTCCCATCCGAGTAGAGGCTTGCAGCGCA 180
 QY 181 AGAATGTCATCGGAGAGTCAATTTGATGAAGAAATCAATATTTGGGAAGCCCAAGCTT 240
 DB 181 AGAATGTCATCGGAGAGTCAATTTGATGAAGAAATCAATATTTGGGAAGCCCAAGCTT 240
 QY 241 GATATCGAGGAGTTTGTGTGACTATTTACGACCGAATCCGGCAAAACGGATGGA 300
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 DB 301 TGGTTTGGAGCACCAGGATTCGCTGTGAGTCAACCGAGCAGCAAGATGATGCGAGTT 360
 QY 361 ATGGGAACGATTTTCGGAAGAAGCAGCGGAAATTTTGAACCTTCTGTGAGCAGCTG 420
 DB 361 ATGGGAACGATTTTCGGAAGAAGCAGCGGAAATTTTGAACCTTCTGTGAGCAGCTG 420
 QY 421 CTCGAGTGGCCAGAAATCTCATTTTCACTGATCAGAGATGTTGGAGCTTGGAAAT 480
 DB 421 CTCGAGTGGCCAGAAATCTCATTTTCACTGATCAGAGATGTTGGAGCTTGGAAAT 480
 QY 481 GCACAGACAGATCAATGCTCAATGTCTTATGACGTTTATGAGTCTAATCTGCTGCG 540
 DB 481 GCACAGACAGATCAATGCTCAATGTCTTATGAGTCTAATCTGCTGCG 540
 QY 541 GGTTCGTAGTGTGAAAGATGATGAGATCCGTGAACTGAGGAGCAACAGTCCAACTC 600
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 DB 601 TTGCTTACACATTCGCTGTTCATCAAAACCGGATCCGCAACATGGAAGAACAAAT 660
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 DB 661 CGGAGCTGGAGCAGCTTCATGACACTCGGAAACAAATGAAGAGAGCTACGAGAGCA 720
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 DB 721 GAAGCTGAAAGTGGGAGCGCGGAGCAGAAACAGACGCTGATGATTTGGCGCTGGA 780
 QY 781 GTAACAGCTGAGCAGATTTGAATCTGTGAGTGTGTGGGAGATGATTTGACG 840
 DB 781 GTAACAGCTGAGCAGATTTGAATCTGTGAGTGTGTGGGAGATGATTTGACG 840
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 DB 841 TTGAAGTAACTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTTGA 900
 QY 901 ATTCATTTTTCGCTCACTGATTTCTTCATTCCTTTGAAGTGAAGAGTGAAGAGTGA 960
 DB 901 ATTCATTTTTCGCTCACTGATTTCTTCATTCCTTTGAAGTGAAGAGTGAAGAGTGA 960
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 DB 961 CCACAATTAAGGCTCTCTGTGCTGATTTGATTTTACTGCAATTTTTCGATTTGCTT 1020
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 DB 1021 TTTTTCGCAAAACCTTAATTCGCGTAATATCAACTTTTCGCTGCTGTGATTTTC 1080
 QY 1081 GTCAAAACCTTAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 DB 1081 GTCAAAACCTTAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140

QY 1141 CATTCGAAGTACCCCTGTATCTCAATATTCATCTTCACTTACGTCTCTTTCGT 1200
 DB 1141 CATTCGAAGTACCCCTGTATCTCAATATTCATCTTCACTTACGTCTCTTTCGT 1200
 QY 1201 GTGGCCTTTCACACTCCGCCCAATTCCTGTAGCGTAGCGGACGCTTGTATTTATTTT 1260
 DB 1201 GTGGCCTTTCACACTCCGCCCAATTCCTGTAGCGTAGCGGACGCTTGTATTTATTTT 1260
 QY 1261 TTCAATGCTTCTCTCTACCAACCAAAAAACGGTTCAAAAA 1315
 DB 1261 TTCAATGCTTCTCTCTACCAACCAAAAAACGGTTCAAAAA 1315

RESULT 8
 US-09-233-527-5
 ; Sequence 5, Application US/09233527
 ; Patent No. 6465617
 ; GENERAL INFORMATION:
 ; APPLICANT: Horvitz, H. Robert
 ; APPLICANT: Hengartner, Michael
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 ; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
 ; FILE REFERENCE: 0197/201004
 ; CURRENT APPLICATION NUMBER: US/09/233,527
 ; PRIOR FILING DATE: 1999-01-20
 ; PRIOR APPLICATION NUMBER: 07/898,933
 ; PRIOR FILING DATE: 1992-06-12
 ; PRIOR APPLICATION NUMBER: 07/927,681
 ; PRIOR FILING DATE: 1992-08-10
 ; PRIOR APPLICATION NUMBER: 08/288,295
 ; PRIOR FILING DATE: 1994-08-10
 ; PRIOR APPLICATION NUMBER: 08/801,248
 ; PRIOR FILING DATE: 1997-02-19
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 1315
 ; TYPE: DNA
 ; ORGANISM: Caenorhabditis elegans
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (7)...(846)
 ; US-09-233-527-5

Query Match 99.8%; Score 1313; DB 4; Length 1315;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAATGACAGCGCTGACGCGGAGCAACACGCTGAGCAATTCGCGCTATCGGAGCA 60
 DB 1 TTGGAATGACAGCGCTGACGCGGAGCAACACGCTGAGCAATTCGCGCTATCGGAGCA 60
 QY 61 ACAGTGGGAGCTGGGAGATGAAGAGTTCCTGGGATTAAGAGCAGACAGCCACCGAT 120
 DB 61 ACAGTGGGAGCTGGGAGATGAAGAGTTCCTGGGATTAAGAGCAGACAGCCACCGAT 120
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 DB 121 TTGGAATCAATAGTAGTCTCAGAGACTTCCCATCCGAGTAGAGGCTTGCAGCGCA 180
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 DB 181 AGAATGTCATCGGAGAGTCAATTTGATGAAGAAATCAATATTTGGGAAGCCCAAGCTT 240
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 DB 301 TGGTTTGGAGCACCAGGATTCGCTGTGAGTCAACCGAGCAGCAAGATGATGCGAGTT 360

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DB 421 CTCGACGTGCCAGATCTCATTTTCTACGTATCAGATGTGGTTCGAGCGTTGGAAAT 480
OY 481 GCACAGACAGATCATATGTCCTATGAGACGTTGATAGGCTATCTGCTGCGC 540
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DB 481 GCATAGACAGATCATATGTCCTATGAGACGTTGATAGGCTATCTGCTGCGC 540
OY 541 GGTTCGTAGCTGCAAAATGATGGAATCCGTGAACTGCAGAGCAAGTCCGAAACCTC 600
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DB 541 GGTTCGTAGCTGCAAAATGATGGAATCCGTGAACTGCAGAGCAAGTCCGAAACCTC 600
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DB 601 TTGCTTTACACATCGCTGTTCACTCAAAACGGGATCCGCAACACTGGAAGAACACAT 660
OY 661 CGGAGCTGGAGACTTCATGACATCGGAAACAAATGAAAGAGGATAGGAAGAGCA 720
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DB 661 CGGAGCTGGAGACTTCATGACATCGGAAACAAATGAAAGAGGATAGGAAGAGCA 720
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DB 721 GAAGCTGAAAAAGTGGAGACGCGGAGACAGACAGCGGTGCGATGATGGCGCTGA 780
OY 781 GTACAGCTGGAGACCTTGGAAATCTGTGAGTCTGCTGTGGCGGATGATGTTCAAC 840
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DB 781 GTACAGCTGGAGACCTTGGAAATCTGTGAGTCTGCTGTGGCGGATGATGTTCAAC 840
OY 841 TTGAAGTAACTGATTCATTTGTGTAATTAATTAATGATGACACTCTTACATTTGA 900
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DB 841 TTGAAGTAACTGATTCATTTGTGTAATTAATTAATGATGACACTCTTACATTTGA 900
OY 901 ATCTCATTTTTCGCTACTGATTTCTGATCTTGAACCTTGAAGTGGGAAAGCTAGG 960
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DB 901 ATCTCATTTTTCGCTACTGATTTCTGATCTTGAACCTTGAAGTGGGAAAGCTAGG 960
OY 961 CCACAAATTAAGGCTCTGTGTGATTTAGATTTTCTGCAATTTTTCGATTTGCT 1020
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DB 961 CCACAAATTAAGGCTCTGTGTGATTTAGATTTTCTGCAATTTTTCGATTTGCT 1020
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DB 1021 TTTTGTGGCCAAACCTTACTGCGGTAAATATCACTTTTCCGTGCTGATTC 1080
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DB 1081 GTCAAAACCTTGAACCTTATTTCTGCGGTGAGCTCCGCTTCCTTCCA 1140
OY 1141 CATTTCCAAAGTACCTGTATCTCAATTAATTCATCTTCACTTTAAGCTCTTTTGT 1200
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DB 1141 CATTTCCAAAGTACCTGTATCTCAATTAATTCATCTTCACTTTAAGCTCTTTTGT 1200
OY 1201 GTGGCTCTTCCAACTCCGCAATTCCTGTAGCTGACGAGATTTGTATTTT 1260
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DB 1201 GTGGCTCTTCCAACTCCGCAATTCCTGTAGCTGACGAGATTTGTATTTT 1260
OY 1261 TTCAAAATGTTTCTCTACAAACAAAAAGGTTCAAAAAA 1315
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DB 1261 TTCAAAATGTTTCTCTACAAACAAAAAGGTTCAAAAAA 1315

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RESULT 9

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; Sequence 6, Application US/09233527
; Patent No. 6465617
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A

```

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; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 01997/201004
; CURRENT APPLICATION NUMBER: US/09/233,527
; CURRENT FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/988,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
; US-09-233-527-6

Query Match          99.8%; Score 1313; DB 4; Length 1315;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTGAGATGACACGCTGACACGCGGCAACACTCGCTGACGAATTCGGCGTATGGCGACGA 60
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DB 121 TTTGGAATCAATAGTAGTACTGACGACTTGCCATCCAGACGAGTAGAGGCTTGCACGCA 180
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DB 241 GATATCGAGGATTTTGGTGCAGCTATTTTCACGACCGAATCCGCAAAACGGAATGGA 300
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DB 361 ATGGGAACGATATTCGAGAAAGACACGCGGAAATTTTGAGACCTTCTGTGAGACGCTG 420
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DB 481 GCACAGACAGATCATATGTCCTAATGTCTATGAGACGTTGATAGTCTAATCTGCTGCGC 540
OY 541 GGTTCGTAGCTGCAAAATGATGGAATCCGTGAACTGCAGAGCAAGTCCGAAACCTC 600
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DB 541 GGTTCGTAGCTGCAAAATGATGGAATCCGTGAACTGCAGAGCAAGTCCGAAACCTC 600
OY 601 TTGCTTTACACATCGCTGTTCACTCAAAACGGGATCCGCAACACTGGAAGAACACAT 660
    |||
DB 601 TTGCTTTACACATCGCTGTTCACTCAAAACGGGATCCGCAACACTGGAAGAACACAT 660
OY 661 CGGAGCTGGAGACTTCATGACATCGGAAACAAATGAAAGAGGATAGGAAGAGCA 720
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Db 661 CGAGCTGGGAGACACTTTCATGACACTCGGAAAAACAATGAAAGAGACTACGAACGAGCA 720
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Db 721 GAAGCTGAAAAAGTGGGAGCGCCGGAAGCAGAACAGACGCGTGGTCATGATTTGGCGCTGGCA 780
QY 781 GTAACAGCTGAGACCACTTGTGGAATCGTTGGAGTCGTCGTGTGGGGGGGATGATGTTCCAGC 840
Db 781 GTAACAGCTGAGACCACTTGTGGAATCGTTGGAGTCGTCGTGTGGGGGGGATGATGTTCCAGC 840
QY 841 TTGAAGTAAACGTAATTCATAATTTGTGTAATAATTAATTTATGTACACACTCCTTACATTTGA 900
Db 841 TTGAAGTAAACGTAATTCATAATTTGTGTAATAATTAATTTATGTACACACTCCTTACATTTGA 900
QY 901 ATCTCATTTTTCGCTACATGATTCCTCATCCTTTGAACTGGAAGAAAGTGGAAAGCTAGG 960
Db 901 ATCTCATTTTTCGCTACATGATTCCTCATCCTTTGAACTGGAAGAAAGTGGAAAGCTAGG 960
QY 961 CCACAAATTTAGCGGCTCTCTGTGTGCAATTTTACGCAATTTTTCGATTTGGCT 1020
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QY 1021 TTTTGTGGCCAAACCCCTACTTTCGCGCGTAATATACATTTTCGTTCTGTACATTTTC 1080
Db 1021 TTTTGTGGCCAAACCCCTACTTTCGCGCGTAATATACATTTTCGTTCTGTACATTTTC 1080
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Db 1081 GTCAAAAACCCCTGAAACCCCTACTTTCGCGCGTGGCCCTAGCTCCGCTCTCTTCCCA 1140
QY 1141 CATTTCCAAAGTACCCCTGTATCTCAATTAATTCATCTTCACTTTAACTGTCTCTTTTGGT 1200
Db 1141 CATTTCCAAAGTACCCCTGTATCTCAATTAATTCATCTTCACTTTAACTGTCTCTTTTGGT 1200
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Db 1201 GGGGCTCTTCCAACTCCGCCCAATTCCTGTACGCGTACGGGACTTGTATTTATTTT 1260
QY 1261 TTCAAAATTTGTTTCTCTCTACACAAACAAAAACGGTTCAAAAAA 1315
Db 1261 TTCAAAATTTGTTTCTCTCTACACAAACAAAAACGGTTCAAAAAA 1315

RESULT 10
US-09-234-186-1
; Sequence 1, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-06-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6559
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: misc_feature

Query Match	48.1%;	Score 632.6;	DB 4;	Length 6559;
Best Local Similarity	99.8%;	Pred. No. 2.9e-190;		
Matches 632;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
US-09-234-186-1				
LOCATION: (1)...:(6559)				
OTHER INFORMATION: n = A,T,C or G				
Query Match	48.1%;	Score 632.6;	DB 4;	Length 6559;
Best Local Similarity	99.8%;	Pred. No. 2.9e-190;		
Matches 632;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
US-09-233-527-1				
Sequence 1, Application US/09233527				
Patent No. 6465617				
GENERAL INFORMATION:				
APPLICANT: Horvitz, H. Robert				
APPLICANT: Hegartner, Michael				
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A				
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND				
FILE REFERENCE: 01997/201004				
CURRENT APPLICATION NUMBER: US/09/233,527				
CURRENT FILING DATE: 1999-01-20				
PRIOR APPLICATION NUMBER: 07/898,933				
PRIOR FILING DATE: 1992-06-12				
PRIOR APPLICATION NUMBER: 07/927,681				
PRIOR FILING DATE: 1992-08-10				
PRIOR APPLICATION NUMBER: 08/288,295				
PRIOR FILING DATE: 1994-08-10				
PRIOR APPLICATION NUMBER: 08/801,248				
669 GGACGACCTTCATGACACCTCGGAAAAACAATGAAAGAGACTACGACGACGAGAACTGA 728				
Db 3392 GGACGACCTTCATGACACCTCGGAAAAACAATGAAAGAGACTACGACGACGAGAACTGA 3451				
QY 729 AAAAGTGGGAGCCCGGAGAGCAAGAACAGAGCGGTGTCATGTATTTGGCCCTGGAGTAACAGC 788				
Db 3452 AAAAGTGGGAGCCCGGAGAGCAAGAACAGAGCGGTGTCATGTATTTGGCCCTGGAGTAACAGC 3511				
QY 789 TGGAGCCATTGGGAATCGTTGAGAGTCGTGTCGTGTGGGCGAGTATGTTCACTTGAAGTA 848				
Db 3512 TGGAGCCATTGGGAATCGTTGAGAGTCGTGTCGTGTGGGCGAGTATGTTCACTTGAAGTA 3571				
QY 849 ACGTTTCAATTTGTGTAAATATTAATTTATGTACAACTCCCTACATTTGAATCTCAT 908				
Db 3572 ACGTTTCAATTTGTGTAAATATTAATTTATGTACAACTCCCTACATTTGAATCTCAT 3631				
QY 909 TTKGCTCACTGATTTCTCATCTTTGAACTGGAAGAAAGTGGGAAAGCTAGGCCACAAT 968				
Db 3632 TTKGCTCACTGATTTCTCATCTTTGAACTGGAAGAAAGTGGGAAAGCTAGGCCACAAT 3691				
QY 969 TAGGCTCTCTGTGTGCGATTTACGATTTTACTGCAATTTTTCGATGTCCTTTT 1028				
Db 3692 TAGGCTCTCTGTGTGCGATTTACGATTTTACTGCAATTTTTCGATGTCCTTTT 3751				
QY 1029 GGCCAAACCTCACTCCGCGTAATATCAACTTTCGCGTGTCTGTACATTTGTCGCAAAA 1088				
Db 3752 GGCCAAACCTCACTCCGCGTAATATCAACTTTCGCGTGTCTGTACATTTGTCGCAAAA 3811				
QY 1089 CCCTGAAACCTTAATCTTTCGCGGTGGCCCTAGCCCTCCGCTCTCTGCAATTTTCCA 1148				
Db 3812 CCCTGAAACCTTAATCTTTCGCGGTGGCCCTAGCCCTCCGCTCTCTGCAATTTTCCA 3871				
QY 1149 AAGTACCCCTGATCTCATTAATATCATCTTCACTTAAGTGTCTTTGGTGGGCTC 1208				
Db 3872 AAGTACCCCTGATCTCATTAATATCATCTTCACTTAAGTGTCTTTGGTGGGCTC 3931				
QY 1209 TTCCAACTCCGCCCAAAATTCCTGTAGCGGTACGCGACTTTGTATTTATTTTTCACAAAT 1268				
Db 3932 TTCCAACTCCGCCCAAAATTCCTGTAGCGGTACGCGACTTTGTATTTATTTTTCACAAAT 3991				
QY 1269 GTTTTCTCTACACAACAACAAAAACGGTTC 1301				
Db 3992 GTTTTCTCTACACAACAACAAAAACGGTTC 4024				

; PRIOR FILING DATE: 1997-02-19
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO: 1
 ; LENGTH: 6559
 ; TYPE: DNA
 ; ORGANISM: Caenorhabditis elegans
 ; FEATURE:
 ; NAME/KEY: misc-feature
 ; LOCATION: (1)...(6559)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-233-527-1

Query Match 48.1% Score 632.6; DB 4; Length 6559;
 Best Local Similarity 99.8%; Pred. No. 2.9e-190;
 Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 669 GGAGCACTTCATGACACTCGGAAAAACAATGAAGAGGACTACGACGAGCAGAGCTGA 728
 DB 3392 GGAGCACTTCATGACACTCGGAAAAACAATGAAGAGGACTACGACGAGCAGAGCTGA 3451
 QY 729 AAAAGTGGAGCGCGGAGACAGACAGCGTGTGTCATGATTTGGCGTGGAGTAAGACG 788
 DB 3452 AAAAGTGGAGCGCGGAGACAGACAGCGTGTGTCATGATTTGGCGTGGAGTAAGACG 3511
 QY 789 TGGAGCCATTGGAATCGTTGAGTGTGTCGTGTGGCGGATGATGTTCACTTGAAGTA 848
 DB 3512 TGGAGCCATTGGAATCGTTGAGTGTGTCGTGTGGCGGATGATGTTCACTTGAAGTA 3571
 QY 849 ACGTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
 DB 3572 ACGTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3631
 QY 909 TTGGCTACGATTTCTGTCATCTTCACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 968
 DB 3632 TTGGCTACGATTTCTGTCATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3691
 QY 969 TACGGCTCTGTGTGATTTACGATTTTACGATTTTTCGATTTTTCGATTTTTCGATTT 1028
 DB 3692 TACGGCTCTGTGTGATTTACGATTTTACGATTTTTCGATTTTTCGATTTTTCGATTT 3751
 QY 1029 GGCCAAACCTTACCTCCGCTAATATCAACTTTTCCGTTCTGTACATTTTCGTAACAA 1088
 DB 3752 GGCCAAACCTTACCTCCGCTAATATCAACTTTTCCGTTCTGTACATTTTCGTAACAA 3811
 QY 1089 CCGTGAACCTTACCTTTTCGCGGTGAGCGTCCGCTCCGCTCCGCTCCGCTCCGCTCC 1148
 DB 3812 CCGTGAACCTTACCTTTTCGCGGTGAGCGTCCGCTCCGCTCCGCTCCGCTCCGCTCC 3871
 QY 1149 AAGTACCCCTGTATCTCAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 1208
 DB 3872 AAGTACCCCTGTATCTCAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 3931
 QY 1209 TTCCAACTCCCCCAAAATTCCTGTACGCGTACGCGACTTTGTATTTATTTTCAAA 1268
 DB 3932 TTCCAACTCCCCCAAAATTCCTGTACGCGTACGCGACTTTGTATTTATTTTCAAA 3991
 QY 1269 GTTTTCTCTTACACACAAAAAAGGTTTC 1301
 DB 3992 GTTTTCTCTTACACACAAAAAAGGTTTC 4024

RESULT 12
 PCT-US93-05651-1
 ; Sequence 1, Application PC/TUS9305651
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: A Gene Which Prevents Programmed Cell Death
 ; NUMBER OF SEQUENCES: 5
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: diskette
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/05651
 ; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6560 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 PCT-US93-05651-1

Query Match 48.1% Score 632.6; DB 5; Length 6560;
 Best Local Similarity 99.8%; Pred. No. 2.9e-190;
 Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 669 GGAGCACTTCATGACACTCGGAAAAACAATGAAGAGGACTACGACGAGCAGAGCTGA 728
 DB 3393 GGAGCACTTCATGACACTCGGAAAAACAATGAAGAGGACTACGACGAGCAGAGCTGA 3452
 QY 729 AAAAGTGGAGCGCGGAGACAGACAGCGTGTGTCATGATTTGGCGTGGAGTAAGACG 788
 DB 3453 AAAAGTGGAGCGCGGAGACAGACAGCGTGTGTCATGATTTGGCGTGGAGTAAGACG 3512
 QY 789 TGGAGCCATTGGAATCGTTGAGTGTGTCGTGTGGCGGATGATGTTCACTTGAAGTA 848
 DB 3513 TGGAGCCATTGGAATCGTTGAGTGTGTCGTGTGGCGGATGATGTTCACTTGAAGTA 3572
 QY 849 ACGTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
 DB 3573 ACGTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3632
 QY 909 TTGGCTACGATTTCTGTCATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 968
 DB 3633 TTGGCTACGATTTCTGTCATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3692
 QY 969 TACGGCTCTGTGTGATTTACGATTTTACGATTTTTCGATTTTTCGATTTTTCGATTT 1028
 DB 3693 TACGGCTCTGTGTGATTTACGATTTTACGATTTTTCGATTTTTCGATTTTTCGATTT 3752
 QY 1029 GGCCAAACCTTACCTCCGCTAATATCAACTTTTCCGTTCTGTACATTTTCGTAACAA 1088
 DB 3753 GGCCAAACCTTACCTCCGCTAATATCAACTTTTCCGTTCTGTACATTTTCGTAACAA 3812
 QY 1089 CCGTGAACCTTACCTTTTCGCGGTGAGCGTCCGCTCCGCTCCGCTCCGCTCCGCTCC 1148
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 QY 1149 AAGTACCCCTGTATCTCAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 1208
 DB 3873 AAGTACCCCTGTATCTCAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 3932
 QY 1209 TTCCAACTCCCCCAAAATTCCTGTACGCGTACGCGACTTTGTATTTATTTTCAAA 1268
 DB 3933 TTCCAACTCCCCCAAAATTCCTGTACGCGTACGCGACTTTGTATTTATTTTCAAA 3992
 QY 1269 GTTTTCTCTTACACACAAAAAAGGTTTC 1301
 DB 3993 GTTTTCTCTTACACACAAAAAAGGTTTC 4025

RESULT 13
 US-08-232-463-14
 ; Sequence 14, Application US/08232463
 ; Patent No. 5670367
 ; GENERAL INFORMATION:
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEIFLINGER, F.
 ; APPLICANT: FALKNER, F. G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 diagonal Road, Suite 500
 ; City: Alexandria
 ; STATE: VA
 ; COUNTRY: USA


```

      ZIP: 22313-0299
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/232,463
      FILING DATE:
      CLASSIFICATION: 435
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/07/935,313
      FILING DATE:
      APPLICATION NUMBER: EP 91 114 300.6
      FILING DATE: 26-AUG-1991
      ATTORNEY/AGENT INFORMATION:
      NAME: BENT, Stephen A.
      REGISTRATION NUMBER: 29,768
      REFERENCE/DOCKET NUMBER: 30472/114 IMMU
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (703)836-9300
      TELEFAX: (703)683-4109
      TELEX: 899149
      INFORMATION FOR SEQ ID NO: 14:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 7218 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      IMMEDIATE SOURCE:
      CLONE: PT29pt-Fls
      US-08-232-463-14

Query Match
Best Local Similarity 6.2%, Score 81.8; DB 1; Length 7218;
Matches 20; Conservative 240; Mismatches 137; Indels 0; Gaps 0;

QY 891 TTACATTGAAATCATTTTGGCCACGATTCCTCATCTTGAACGTGAAGAGCTGG 950
DB 1067 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1126
QY 951 GAAAGCTAGGCCAATAATTAGGCTCTGTGATTTAGATTTACGCAATTTT 1010
DB 1127 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1186
QY 1011 CGATTGCTTTTGGCCAAACCTCTCTCCGGTAATCACTTTTCCGTTTC 1070
DB 1187 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1246
QY 1071 TGTACATTTGCTCAAAAACCTGAAACCTAATCTTCTGCGCGTGGCCAGCTCCGC 1130
DB 1247 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1306
QY 1131 TTCTCTCCATTTCCAAAGTACCCCTGTATCTCAATATTCATCTTCACTTAAGT 1190
DB 1307 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1366
QY 1191 CTCTTTCTGTGGCCCTCTCAACCTCCCAATTCCTGTAAGGCTACGCACTTGT 1250
DB 1367 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1426
QY 1251 ATTATTTTTCAAATGTTTCTCTGTAACAAC 1287
DB 1427 YYYYYYGTACCAATCTCTATCTCTTAACTAC 1463

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      APPLICANT: FALKNER, F. G.
      TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
      NUMBER OF SEQUENCES: 52
      CORRESPONDENCE ADDRESS:
      ADDRESSEE: Foley & Lardner
      STREET: 1800 Diagonal Road, Suite 500
      CITY: Alexandria
      STATE: VA
      COUNTRY: USA
      ZIP: 22313-0299
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/232,463
      FILING DATE:
      CLASSIFICATION: 435
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/07/935,313
      FILING DATE:
      APPLICATION NUMBER: EP 91 114 300.6
      FILING DATE: 26-AUG-1991
      ATTORNEY/AGENT INFORMATION:
      NAME: BENT, Stephen A.
      REGISTRATION NUMBER: 29,768
      REFERENCE/DOCKET NUMBER: 30472/114 IMMU
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (703)836-9300
      TELEFAX: (703)683-4109
      TELEX: 899149
      INFORMATION FOR SEQ ID NO: 14:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 7218 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      IMMEDIATE SOURCE:
      CLONE: PT29pt-Fls
      US-08-232-463-14

Query Match
Best Local Similarity 4.2%, Score 55.6; DB 1; Length 7218;
Matches 13; Conservative 222; Mismatches 151; Indels 0; Gaps 0;

QY 36 GACGAATCCGGCTATGCGGACGACGATGCGGACGAGATGAGAGCTTCTGG 95
DB 1427 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1368
QY 96 GATAAAGGACAGAGCCCACTTTTGAATCAATAGTATGCTGAGACTTGCATC 155
DB 1367 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1308
QY 156 ACCGATAGCAGCTTCGACGCGCAAGATGTCATCGAGAGCTCATTTGAGAAAAT 215
DB 1307 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1248
QY 216 CAATGATGGAGAGCAAGCAAGCTTGATATCGAGGATTTGTGCTGACTATTACCA 275
DB 1247 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1198
QY 276 CGAATCCGCAAAAGGATGGAATGTTGGACACCGGATTCGCTGTGAGTGCA 335
DB 1187 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1128
QY 336 ACCGAGACAGAAAGATGCGAGTATGGAAGCAATATTCGAGAAAGACGCGGAAA 395
DB 1127 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1068
QY 396 TTTGAGACCTTCTGTGAGCAGCTGC 421
DB 1067 RATCGCAAGCTCTGCTGACCTGCAGC 1042

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RESULT 15
US-09-007-005-17/c
; Sequence 17, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Robertis, Richard W.
; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007, 005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035, 963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064, 491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; NAME/KEY: misc-feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17

Query Match          3 6%; Score 47.6; DB 4; Length 289;
Best Local Similarity 11.7%; Pred No. 2.4e+05;
Matches 32; Conservative 107; Mismatches 135; Indels 0; Gaps 0;

QY      1006 TTTTCCGATTCGGCTTTTTTTTTTGCCAAACCCCTACTTCGCCGTAAATCACTTTCCG 1065
           |||||  ||  |||||||||  |::: |: : : : : : : : : : : : : : : : : : :
DB      287 TTTTTTTTTTTTTTTTTTTTTTTTAAVGYCYCAVAVGYAAYTYTAAVCYGAYA 228
           |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY      1066 TGTTCTGTACATTTCGCAGAAAACCCTGAACCCCTAACCTTTTCGGCGGCTAGCCT 1125
           ::: | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      227 YGYCYTATGYGSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSN 168
           : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      1126 CCGCGTCTCTCCACCATTCACAAGTACCCTGTATCATCAATAATTCATCTTCACTTA 1185
           : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      167 YNYSYNNYNSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSN 108
           : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      1186 ACTGTCCTCTTTCGTGTGGCCTCTTCCAACCTCCCCCAAATTCCTGTAGCGGTAGCGGAC 1245
           ::: | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      107 YNYSYNNYNSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSNNYSN 48
           : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      1246 TTTCGATTAATTTTTTTCGAATCTGTTCTCTCT 1279
           : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      47 YTAATATTTTGYTAATATTAATTAAGTAAAT 14
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Job time : 73.2432 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 03:32:51 ; Search time 130.582 Seconds
(without alignments)
6280.048 Million cell updates/sec

Title: US-09-993-420A-2

Perfect score: 1315
Sequence: 1 tttagatgacacgctgcac.....cgttcaaaaaaaaaa 1315

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 460893 seqs, 311809382 residues

Total number of hits satisfying chosen parameters: 921786

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	42	3.2	3160	US-10-098-841-273	Sequence 273, App
2	41	3.1	2000	US-09-938-842A-3764	Sequence 3764, App
3	39.8	3.0	425	US-09-834-975-451	Sequence 451, App
4	39.8	3.0	425	US-09-834-975-451	Sequence 451, App
5	39.6	3.0	458	US-09-770-444-474	Sequence 474, App
6	39.4	3.0	1680	US-09-986-480-20	Sequence 20, Appl
7	38.6	2.9	418	US-09-960-352-4845	Sequence 4845, App
8	38	2.9	608	US-09-770-145-894	Sequence 894, App
9	37	2.8	312	US-09-960-352-8414	Sequence 8414, App
10	37	2.8	410	US-09-960-352-4438	Sequence 4438, App
11	37	2.8	630	US-09-925-300-548	Sequence 548, App
12	37	2.8	180216	US-09-835-232-6	Sequence 6, Appl
13	36.8	2.8	387	US-09-867-701-10218	Sequence 10218, A
14	36.8	2.8	459	US-10-015-219-777	Sequence 777, App
15	36.8	2.8	459	US-09-777-564-777	Sequence 777, App
16	36.8	2.8	517	US-10-015-219-1649	Sequence 1649, App
17	36.8	2.8	517	US-09-777-564-1649	Sequence 1649, App
18	36.8	2.8	566	US-09-796-692-4903	Sequence 4903, App
19	36.8	2.8	727	US-10-202-193-281	Sequence 281, App

C 20	36.8	2.8	751	9	US-10-202-193-280	Sequence 280, App
C 21	36.8	2.8	773	9	US-10-202-193-176	Sequence 176, App
C 22	36.8	2.8	2361	10	US-09-925-299-59	Sequence 59, Appl
C 23	36.6	2.8	396	9	US-09-970-966-10	Sequence 10, Appl
C 24	36.6	2.8	396	10	US-09-825-294-10	Sequence 10, Appl
C 25	36.4	2.8	312	10	US-09-960-352-8414	Sequence 8414, App
C 26	36.4	2.8	742	9	US-09-950-938-35	Sequence 35, Appl
C 27	36	2.7	1531	10	US-09-925-300-577	Sequence 577, App
C 28	35.8	2.7	221	10	US-09-864-761-18315	Sequence 18315, A
C 29	35.8	2.7	487	10	US-09-864-761-1556	Sequence 1556, App
C 30	35.6	2.7	253	10	US-09-778-320-124	Sequence 124, App
C 31	35.6	2.7	253	10	US-09-910-689-124	Sequence 124, App
C 32	35.6	2.7	253	12	US-10-010-742-124	Sequence 124, App
C 33	35.6	2.7	373	10	US-09-960-352-1676	Sequence 1676, A
C 34	35.6	2.7	202001	10	US-09-734-674-3	Sequence 3, Appl
C 35	35.4	2.7	1307	10	US-09-250-611-3	Sequence 3, Appl
C 36	35.4	2.7	2000	9	US-09-938-842A-2926	Sequence 2926, App
C 37	35.4	2.7	4019	10	US-09-764-847-1431	Sequence 1431, App
C 38	35.2	2.7	160	10	US-09-783-590-3161	Sequence 3161, App
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C 40	35	2.7	308	10	US-09-960-352-7670	Sequence 7670, App
C 41	35	2.7	1043	10	US-09-925-302-53	Sequence 53, Appl
C 42	34.8	2.6	392	10	US-09-960-352-2634	Sequence 2634, App
C 43	34.8	2.6	416	10	US-09-960-352-4584	Sequence 4584, App
C 44	34.8	2.6	418	10	US-09-960-352-4845	Sequence 4845, App
C 45	34.8	2.6	424	10	US-09-960-352-11218	Sequence 11218, A

ALIGNMENTS

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; Sequence 273, Application US/10098841
; Publication No. US20020197679A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhao, Qian A.
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20020197679A1 Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/10/098,841
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: pt_Fligenes Version 1.0
; SEQ ID NO 273
; LENGTH: 3160
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (169)..(1092)
; US-10-098-841-273

Thu. Mar 6 08:14:04 2003

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; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurdan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09/770,444
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-444-474

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; Publication No. US20030027999A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 143 Human Secreted Proteins
; FILE REFERENCE: PS500P1
; CURRENT APPLICATION NUMBER: US/09/986,480
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/12788
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/134,068
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 456
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; NAME/KEY: SITE

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; LOCATION: (1674)
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; Sequence 4845, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengding
; APPLICANT: Byatt, John C.
; APPLICANT: Machialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4845
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 21-LIB3058-035-Q1-K1-F9
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RESULT 8
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; Sequence 894, Application US/09770149
; Patent No. US2002005963A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.

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QY 1306	AAAAAAAAA	1314		
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[illegible]

Thu Mar 6 08:14:04 2003

us-09-993-420a-2.rnpb

Page 6

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GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-993-420A-2

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Listing first 45 summaries

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19	1313	99.8	1315	US-08-466-194-14	Sequence 14, Appli
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OTHER INFORMATION: /product= "Ced-9"

US-07-927-681-2

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	Indels 0;	Gaps 0;

Maçines 1310, Conservatório de Música, 60

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C	45	45.8	3.5	569	64	US-60-207-458-121823	Sequence 121823, A

ALIGNMENTS

RESULT 1
US-07-927-681-2
Sequence 3 Application NS/07927681

GENERAL INFORMATION:

APPLICANT: Horvitz, H. Robert
APPLICANT: Hengartner, Michael
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL
TITLE OF INVENTION: DEATH AND USES THEREFOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

OTHER INFORMATION: /product= "Cd-9"									
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Db	181	AGCATGTCATGAGAGAGTCAATTATGAAAAATCAATGATTTGGGAAGACCAAGGCTT	240						
OY	241	GATATCGAGGATTTGTGCTGCACATATTTACGACCGCATCCGGCAAAAGCAATGGAA	300						
Db	241	GATATCGAGGATTTGTGCTGCACATATTTACGACCGCATCCGGCAAAAGCAATGGAA	300						
OY	301	TGGTTTGGAGCACCGGAGTTGCCGTGAGTGCACACCGAGCACGAATGATGCGAGTT	360						
Db	301	TGGTTTGGAGCACCGGAGTTGCCGTGAGTGCACACCGAGCACGAATGATGCGAGTT	360						
OY	361	ATGGGAACGATATTTCGAGAAGAACGACCGCGGAAATTTTGAACCTCTGTGAGAGCTG	420						
Db	361	ATGGGAACGATATTTCGAGAAGAACGACCGCGGAAATTTTGAACCTCTGTGAGAGCTG	420						
OY	421	CTGGCAGTGGCCGAAATTCATTTTACTGATACAGATGTTGGTTCGACGGTTGGAAT	480						
Db	421	CTGGCAGTGGCCGAAATTCATTTTACTGATACAGATGTTGGTTCGACGGTTGGAAT	480						
OY	481	GCACAGACAGATCAATGTCCAAATGTCTTATGACGTTTGAATAGTCTAATTCGTTCGGC	540						
Db	481	GCACAGACAGATCAATGTCCAAATGTCTTATGACGTTTGAATAGTCTAATTCGTTCGGC	540						
OY	541	GCTTTCGACTCGAAAAATGATGGAATCCGTGAACTGAGGAGCAAGTGGCAAACTTC	600						
Db	541	GCTTTCGACTCGAAAAATGATGGAATCCGTGAACTGAGGAGCAAGTGGCAAACTTC	600						
OY	601	TTGCTTTACACATCGCTGTTCATCAAAAACGCGATCCGACAACTTGAAGAAACCAAT	660						
Db	601	TTGCTTTACACATCGCTGTTCATCAAAAACGCGATCCGACAACTTGAAGAAACCAAT	660						
OY	661	CGAGCTGGGACGACTTCATGACACTCGGAAAAAATGAAGAAAGAGCACTACGAACGACA	720						
Db	661	CGAGCTGGGACGACTTCATGACACTCGGAAAAAATGAAGAAAGAGCACTACGAACGACA	720						
OY	721	GAGCTGAAAAAAGTGGGACGCGCGGAAGCAGAACGACGCTGTGCATGATTTGGCGCTGGA	780						
Db	721	GAGCTGAAAAAAGTGGGACGCGCGGAAGCAGAACGACGCTGTGCATGATTTGGCGCTGGA	780						
OY	781	GTAACAGTGAACCATTTGGAATGCTTGCATGATGCTGCTGCTGGGCGGATATTTCAGC	840						
Db	781	GTAACAGTGAACCATTTGGAATGCTTGCATGATGCTGCTGCTGGGCGGATATTTCAGC	840						
OY	841	TTGAAGTAAACGATTAATTTGTGTAATTAATTAATTTATGATACACTCTTACATTTGA	900						
Db	841	TTGAAGTAAACGATTAATTTGTGTAATTAATTAATTTATGATACACTCTTACATTTGA	900						
OY	901	ATCTCATTTTTCCTACTGATTTCTCTCACTCTTTGAACGTGAAGAGTGGAAAAAGCTAGG	960						
Db	901	ATCTCATTTTTCCTACTGATTTCTCTCACTCTTTGAACGTGAAGAGTGGAAAAAGCTAGG	960						
OY	961	CCACAAATTAGGCTCTCTGTGCATTTAGCATTTTACTCAATTTTTCGATTCCT	1020						
Db	961	CCACAAATTAGGCTCTCTGTGCATTTAGCATTTTACTCAATTTTTCGATTCCT	1020						

Db 961 CCACAAATTAAGGCTCTCTGTGATTTAGCATTTTTCAGATTTTTCGATGGCT 1020
 QY 1021 TTTTGTGGCCAAACCCCTACTTCCGGTAATATCAATTTTCCGTCTGTACATTC 1080
 Db 1021 TTTTGTGGCCAAACCCCTACTTCCGGTAATATCAATTTTCCGTCTGTACATTC 1080
 QY 1081 GTCAAAAACCCCTGAACCCCTAATTTTCTGCGCGTGGCCCTACGCTCCGCTCTCTCCA 1140
 Db 1081 GTCAAAAACCCCTGAACCCCTAATTTTCTGCGCGTGGCCCTACGCTCCGCTCTCTCCA 1140
 QY 1141 CATTTCAAGTACCCCTGTATCTCAATTAATTCATCTTCACTTAACTGTCTCTTTCGT 1200
 Db 1141 CATTTCAAGTACCCCTGTATCTCAATTAATTCATCTTCACTTAACTGTCTCTTTCGT 1200
 QY 1201 GTGGCCCTTTCACACTCCGCCAAATTCCTGTAGCGGTACGAGCATTTGATTTATTTT 1260
 Db 1201 GTGGCCCTTTCACACTCCGCCAAATTCCTGTAGCGGTACGAGCATTTGATTTATTTT 1260
 QY 1261 TTCAAAATTTTCTCTCTCAACAACAACAAAAACGGTTCAAAAAA 1315
 Db 1261 TTCAAAATTTTCTCTCTCAACAACAACAAAAACGGTTCAAAAAA 1315

RESULT 2

US-08-288-295-2

Sequence 2, Application US/08288295

GENERAL INFORMATION:

APPLICANT: Horvitz, H. Robert

APPLICANT: Hengartner, Michael

TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A

TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & RICHARDSON

STREET: 225 Franklin Street, Suite 3100

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A. (F) ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/288,295

FILING DATE: 10-AUG-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/927,681

FILING DATE: 10-AUG-1992

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 01997/201003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1315 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

FEATURE:

NAME/KEY: CDS

LOCATION: 7..846

OTHER INFORMATION: /product= "Ced-9"

US-08-288-295-2

Query Match 100.0%; Score 1314.6; DB 6; Length 1315;
 Best Local Similarity 100.0%; Pred. No. 1.5e-288;
 Matches 1315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGAGATGACACGCTGACGCGGACAACTGCTGACGAATCCGGCATGCGGACGA 60
 Db 1 TTTGAGATGACACGCTGACGCGGACAACTGCTGACGAATCCGGCATGCGGACGA 60
 QY 61 ACAGTGGCAGCTGGCGAGATGGAAGAGTTTCTGGGGATTAAGGACACAGCCCGAT 120
 Db 61 ACAGTGGCAGCTGGCGAGATGGAAGAGTTTCTGGGGATTAAGGACACAGCCCGAT 120
 QY 121 TTTGGAATCAATAGTATGCTCAGAGCTTGGCATACAGAGTAGGACGCTTTCAGCG 180
 Db 121 TTTGGAATCAATAGTATGCTCAGAGCTTGGCATACAGAGTAGGACGCTTTCAGCG 180
 QY 181 AGAATGTCATCGAGAGAGTCAATTTATGGAATAATCAATGATTTGGGAAGCCAAAGCTT 240
 Db 181 AGAATGTCATCGAGAGAGTCAATTTATGGAATAATCAATGATTTGGGAAGCCAAAGCTT 240
 QY 241 GATATCGAGAGGATTTGTGTCAGCTATTTCACGACCGCAATCCGGCAAAACGGAATGGA 300
 Db 241 GATATCGAGAGGATTTGTGTCAGCTATTTCACGACCGCAATCCGGCAAAACGGAATGGA 300
 QY 301 TGGTTTGAGACACCGGAGATTCCCGTGTGAGTGCACACCGACGACGAATGATCGAGTT 360
 Db 301 TGGTTTGAGACACCGGAGATTCCCGTGTGAGTGCACACCGGACGACGAATGATCGAGTT 360
 QY 361 ATGGGAACGATATTCGACAAAGACACGCGGCAAAATTTTGAACCTTCTGTGACACCTG 420
 Db 361 ATGGGAACGATATTCGACAAAGACACGCGGCAAAATTTTGAACCTTCTGTGACACCTG 420
 QY 421 CTCGAGTGCCCAAGATCTCAATTTTCACTGATGAGATGATGTTTGGAGCGTTGGAAT 480
 Db 421 CTCGAGTGCCCAAGATCTCAATTTTCACTGATGAGATGATGTTTGGAGCGTTGGAAT 480
 QY 481 GCACAGACAGATCAATGTCACAAATGCTTATGAGAGCTTTGATAGGTTAATCTGTTCCGC 540
 Db 481 GCACAGACAGATCAATGTCACAAATGCTTATGAGAGCTTTGATAGGTTAATCTGTTCCGC 540
 QY 541 GGTTCGTAGCTGCAAAATGATGAGAAATCCGTGGAATCGAGGACAAAGTGCAGAACCTC 600
 Db 541 GGTTCGTAGCTGCAAAATGATGAGAAATCCGTGGAATCGAGGACAAAGTGCAGAACCTC 600
 QY 601 TTGCTTTACACATCGCTGTTTCAATCAAAACCGGATCCGCAACCTGGAAGAACCAAT 660
 Db 601 TTGCTTTACACATCGCTGTTTCAATCAAAACCGGATCCGCAACCTGGAAGAACCAAT 660
 QY 661 CGGAGCTGGAGACATTCATGACACTCGGAAACCAATGAAGACGACTACGAAACGAGA 720
 Db 661 CGGAGCTGGAGACATTCATGACACTCGGAAACCAATGAAGACGACTACGAAACGAGA 720
 QY 721 GAAGCTGAAAAAGTGGAGCCCGGAAGACAGACAGCGGTGTCATGATTTGGCGTGA 780
 Db 721 GAAGCTGAAAAAGTGGAGCCCGGAAGACAGACAGCGGTGTCATGATTTGGCGTGA 780
 QY 781 GTAAACGCTGGAGCCCAATGGAATCGTTGAGTGTGTGTGGCGGATGATTTTCACG 840
 Db 781 GTAAACGCTGGAGCCCAATGGAATCGTTGAGTGTGTGTGGCGGATGATTTTCACG 840
 QY 841 TTGAAGTAAAGTAATTAATTTGTAATTAATTTTGAACAACCTTACATTTGA 900
 Db 841 TTGAAGTAAAGTAAATTTGTAATTAATTTTGAACAACCTTACATTTGA 900
 QY 901 ATCTCATTTTTCCTCAGTATTTCTCATCTTTGAACGGAAGAGGGAAGACTAGG 960
 Db 901 ATCTCATTTTTCCTCAGTATTTCTCATCTTTGAACGGAAGAGGGAAGACTAGG 960
 QY 961 CCACAAATTAAGGCTCTCTGTGATTTAGCATTTTTCGATTTTCCGATTTGCT 1020
 Db 961 CCACAAATTAAGGCTCTCTGTGATTTAGCATTTTTCGATTTTCCGATTTGCT 1020
 QY 1021 TTTTGTGGCCAAACCCCTACTTCCGGTAATATCAATTTTCCGATTTGCT 1080

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Db 1021 TTTTGGGCAACCTACTCTCGGTAAATCAACTTTCGCTGTCTGACATTC 1080
Oy 1081 GTCAAAAACCCCTGAACCCCTAATCTTCTCGCGCTGAGCTCCGCTTCCTTCCA 1140
Db 1081 GTCAAAAACCCCTGAACCCCTAATCTTCTCGCGCTGAGCTCCGCTTCCTTCCA 1140
Oy 1141 CATTTCCAAAGTACCCCTGATCTCAATATTCATCTTCACTTACCTGCTCTTTCGT 1200
Db 1141 CATTTCCAAAGTACCCCTGATCTCAATATTCATCTTCACTTACCTGCTCTTTCGT 1200
Oy 1201 GTGGCTCTTCCAACTCCCGCCAAATTCCTGTAGCGGTAGCGGACTTGTATTTT 1260
Db 1201 GTGGCTCTTCCAACTCCCGCCAAATTCCTGTAGCGGTAGCGGACTTGTATTTT 1260
Oy 1261 TTCAATTTGTTTCTCTCTACCAACAACAAAAACGGTTCAAAAA 1315
Db 1261 TTCAATTTGTTTCTCTCTACCAACAACAAAAACGGTTCAAAAA 1315

RESULT 3
US-08-801-248-2
Sequence 2, Application US/08801248
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Hengartner, Michael
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
TITLE OF INVENTION: CELL DEATH AND USES THEREFOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FISH & RICHARDSON
STREET: 225 Franklin Street, Suite 3100
City: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,248
FILING DATE: 19-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/288,295
FILING DATE: 10-AUG-1994
APPLICATION NUMBER: US 07/927,681
FILING DATE: 10-AUG-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 01997/201003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1315 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 7..846
OTHER INFORMATION: /product= "Ced-9"
US-08-801-248-2

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Query Match 100.0%; Score 1314.6; DB 12; Length 1315;
Best Local Similarity 100.0%; Pred. No. 1.5e-288;
Matches 1315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TTTGAGATGACAGCTGACAGCGGAGCAACTGCTGACGAAATCCGCGTATGCGGACGA 60
Db 1 TTTGAGATGACAGCTGACAGCGGAGCAACTGCTGACGAAATCCGCGTATGCGGACGA 60
Oy 61 ACGATGCGAGCTGCGGAGATGAAAGAGATTTCTGGGATTAAGGCAAGCCAGCCAGT 120
Db 61 ACGATGCGAGCTGCGGAGATGAAAGAGATTTCTGGGATTAAGGCAAGCCAGCCAGT 120
Oy 121 TTGGAATTCATATGATGATGCTCAGAGCTTGCATTCACCGAGTATGAGGAGGCTTGCAGCGA 180
Db 121 TTGGAATTCATATGATGATGCTCAGAGCTTGCATTCACCGAGTATGAGGAGGCTTGCAGCGA 180
Oy 181 AGAATGTCATGAGAGTCAATTTGATGAAAAATCAATATTTGGGAAAGGCCAATGCGCTT 240
Db 181 AGAATGTCATGAGAGTCAATTTGATGAAAAATCAATATTTGGGAAAGGCCAATGCGCTT 240
Oy 241 GATATCGAGGATTTGGTGTGACTATTTACGACCGCAATCCGGCAAAACGGAATGGAA 300
Db 241 GATATCGAGGATTTGGTGTGACTATTTACGACCGCAATCCGGCAAAACGGAATGGAA 300
Oy 301 TGGTTTGAGGACCGGAGATTGCGGTGAGTGCACCCGAGCAGCAATGATGCGGAGTT 360
Db 301 TGGTTTGAGGACCGGAGATTGCGGTGAGTGCACCCGAGCAGCAATGATGCGGAGTT 360
Oy 361 ATGGAAACGATATTCGAAAGACAGCGGAAATTTTGGAGCCTTCTGTAGCAGCTG 420
Db 361 ATGGAAACGATATTCGAAAGACAGCGGAAATTTTGGAGCCTTCTGTAGCAGCTG 420
Oy 421 CTCGAGTGCACAGAAATCTATTTTCACTGTATGAGATGTGTTGCGAGGTTGGAAAT 480
Db 421 CTCGAGTGCACAGAAATCTATTTTCACTGTATGAGATGTGTTGCGAGGTTGGAAAT 480
Oy 481 GCACAGACAGATCAATGTCATATCTATGAGCTTATGATGCTATCTGTTGCGC 540
Db 481 GCACAGACAGATCAATGTCATATCTATGAGCTTATGATGCTATCTGTTGCGC 540
Oy 541 GGTTCGTAGTGTCAAAAATGATGAAATCCGTGAAATCCGTGAAATCCGTGAAATCC 600
Db 541 GGTTCGTAGTGTCAAAAATGATGAAATCCGTGAAATCCGTGAAATCCGTGAAATCC 600
Oy 601 TTGCTTACATCGCTGTTCAATCAAAACGCGGATCCGAACTGGAGAGACACAT 660
Db 601 TTGCTTACATCGCTGTTCAATCAAAACGCGGATCCGAACTGGAGAGACACAT 660
Oy 661 CGGAGCTGGAGAGCTTCAATGACACTCGGAAACAAATGAAGAGACTAGCAAGAGCA 720
Db 661 CGGAGCTGGAGAGCTTCAATGACACTCGGAAACAAATGAAGAGACTAGCAAGAGCA 720
Oy 721 GAAGCTGAAAAAGTGGAGCCCGGAAGCAACAGACGCTGCTCATGATTTGGCGCTGGA 780
Db 721 GAAGCTGAAAAAGTGGAGCCCGGAAGCAACAGACGCTGCTCATGATTTGGCGCTGGA 780
Oy 781 GTAAACAGCTGAGCCATGGAATCGTTGGAGTGTGCTGTGGCGGATGATGTTCAAC 840
Db 781 GTAAACAGCTGAGCCATGGAATCGTTGGAGTGTGCTGTGGCGGATGATGTTCAAC 840
Oy 841 TTGAAGTAACGTATTCATTTGTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
Db 841 TTGAAGTAACGTATTCATTTGTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
Oy 901 ATCTCATTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 ATCTCATTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Oy 961 CCACAAATTAAGGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
Db 961 CCACAAATTAAGGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
Oy 1021 TTTTGGCAAAACCTACTTCCGCTGATATCAACTTTCGCTGTCTGTATCAATTC 1080

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Db 1021 TTTTGGGCAACCTACTCCGCTATATCACTTTTCGTTCTGTACATTTTC 1080
Qy 1081 GTCAAAAACCCGAAACCTACTTTTCTGCGCGCTGACCTCCCGCTTCTTCCA 1140
Db 1081 GTCAAAAACCCGAAACCTACTTTTCTGCGCGCTGACCTCCCGCTTCTTCCA 1140
Qy 1141 CATTTCAAAAGTACCCCTGTATCTCAATAATTCATCTTCACTTAACTGCTCTTTCGT 1200
Db 1141 CATTTCAAAAGTACCCCTGTATCTCAATAATTCATCTTCACTTAACTGCTCTTTCGT 1200
Qy 1201 GTGGCCTTCCACCTCCCGCAATTCGTGACGCGTACGCGACTTTGATTTATTTT 1260
Db 1201 GTGGCCTTCCACCTCCCGCAATTCGTGACGCGTACGCGACTTTGATTTATTTT 1260
Qy 1261 TTCAAAATGTTTCTCTCTACACACAAACAAAGGTTCAAAAACCAAAAAA 1315
Db 1261 TTCAAAATGTTTCTCTCTACACACAAACAAAGGTTCAAAAACCAAAAAA 1315

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RESULT 4

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US-09-993-420a-2
: Sequence 2, Application US/09993420A
: GENERAL INFORMATION:
: APPLICANT: Horvitz, H. Robert
: APPLICANT: Hengartner, Michael
: TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
: TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: 01997/201006
: CURRENT APPLICATION NUMBER: US/0993,420A
: PRIOR FILING DATE: 5001-11-09
: PRIOR APPLICATION NUMBER: 09/234,186
: PRIOR FILING DATE: 1999-01-20
: PRIOR APPLICATION NUMBER: 07/898,933
: PRIOR FILING DATE: 1992-06-12
: PRIOR APPLICATION NUMBER: 07/927,681
: PRIOR FILING DATE: 1992-08-10
: PRIOR APPLICATION NUMBER: 08/288,295
: PRIOR FILING DATE: 1994-08-10
: PRIOR APPLICATION NUMBER: 08/801,248
: PRIOR FILING DATE: 1997-02-19
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 1315
: TYPE: DNA
: ORGANISM: Caenorhabditis elegans
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (7)...(846)
: US-09-993-420a-2

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Query Match      100.0%; Score 1314.6; DB 37; Length 1315;
Best Local Similarity 100.0%; Pred. No. 1.5e-288;
Matches 1315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TTTGAGATGACACCTGACGCGGACGACACACGCTGACGATCCGCGATGCGGAGCA 60
Db 1 TTTGAGATGACACCTGACGCGGACGACACACGCTGACGATCCGCGATGCGGAGCA 60
Qy 61 ACGATGGCGACCTGGCGAGATGAAGAGTTTCTGGGATATAAAGGCAACAAGCCACCGAT 120
Db 61 ACGATGGCGACCTGGCGAGATGAAGAGTTTCTGGGATATAAAGGCAACAAGCCACCGAT 120
Qy 121 TTTGGAATCAATAGTATGCTCAGACTTGCATCAACGAGTAGAGAGGCTTCGACGCA 180
Db 121 TTTGGAATCAATAGTATGCTCAGACTTGCATCAACGAGTAGAGAGGCTTCGACGCA 180
Qy 181 AGAATGTCATCGAGAGTCAATTTGATGAAAAATCAATGATTTGGAGAGCAAGGCTT 240
Db 181 AGAATGTCATCGAGAGTCAATTTGATGAAAAATCAATGATTTGGAGAGCAAGGCTT 240

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Qy 241 GATATGAGGAGATTGTGTGACTATTTCACGACCGAATCCGGCAAAACGGAATGAA 300
Db 241 GATATGAGGAGATTGTGTGACTATTTCACGACCGAATCCGGCAAAACGGAATGAA 300
Qy 301 TGGTTTGAGGACCGGGAATTCGCGTGTGAGTCAACCGGAGCAGCAAAATGATGCA 360
Db 301 TGGTTTGAGGACCGGGAATTCGCGTGTGAGTCAACCGGAGCAGCAAAATGATGCA 360
Qy 361 ATGGAGAGATATTCGAGAAAGACACGCGGAAATTTTGAACCTTGTGAGCAGCTG 420
Db 361 ATGGAGAGATATTCGAGAAAGACACGCGGAAATTTTGAACCTTGTGAGCAGCTG 420
Qy 421 CTGCGAGTGGCCAGAAATCTCATTTTCACTGTATCAGAGATGTTGGAGGAGTTGGAAT 480
Db 421 CTGCGAGTGGCCAGAAATCTCATTTTCACTGTATCAGAGATGTTGGAGGAGTTGGAAT 480
Qy 481 GCACGACAGATCAATATGCTCAATGTCTTATGACGTTTGAATGATGATCTATCTTCCG 540
Db 481 GCACGACAGATCAATATGCTCAATGTCTTATGACGTTTGAATGATGATCTATCTTCCG 540
Qy 541 GGTTCGTAGCTCAAAAATGATGAAATCGTGAATCGGAAACGACGCAAGTGGAAACCTC 600
Db 541 GGTTCGTAGCTCAAAAATGATGAAATCGTGAATCGGAAACGACGCAAGTGGAAACCTC 600
Qy 601 TTTGTTTACATTCCTGTTTCAATCAAAAACGCGATCCGCAACACTGGAAGAACACAT 660
Db 601 TTTGTTTACATTCCTGTTTCAATCAAAAACGCGATCCGCAACACTGGAAGAACACAT 660
Qy 661 CGAGCTGGGACGACTTCAATGACACGCGGAAACGAAATGAAAGAGACTACGAACAGCA 720
Db 661 CGAGCTGGGACGACTTCAATGACACGCGGAAACGAAATGAAAGAGACTACGAACAGCA 720
Qy 721 GAAGCTGAAAAGTGGGACCGCGAAGCAAGAACAGCGTGTGATGATGAGGCGTGA 780
Db 721 GAAGCTGAAAAGTGGGACCGCGAAGCAAGAACAGCGTGTGATGATGAGGCGTGA 780
Qy 781 GTAACAGCTGAGGACATTTGGAATTCGTTGAGTCTGTGTGCGGCGAGATGTTGACG 840
Db 781 GTAACAGCTGAGGACATTTGGAATTCGTTGAGTCTGTGTGCGGCGAGATGTTGACG 840
Qy 841 TTGAAGTAACGTAATTAATTTGTAATTAATTAATTAATTAATTAATTAATTAATTA 900
Db 841 TTGAAGTAACGTAATTAATTTGTAATTAATTAATTAATTAATTAATTAATTAATTA 900
Qy 901 ATCTGATTTTGTCTACGATTTCTCATCTTGAACCTGGAAGAGTGGAAAGCTAGG 960
Db 901 ATCTGATTTTGTCTACGATTTCTCATCTTGAACCTGGAAGAGTGGAAAGCTAGG 960
Qy 961 CCACAATTTAGGCTCTGTGTGATTTAGGATTTTACTGCAATTTTTCGATTTGCT 1020
Db 961 CCACAATTTAGGCTCTGTGTGATTTAGGATTTTACTGCAATTTTTCGATTTGCT 1020
Qy 1021 TTTTGGGCAAAACCTTACCTCCGGTAATPACAACTTTCCGTTCTGTACATTTT 1080
Db 1021 TTTTGGGCAAAACCTTACCTCCGGTAATPACAACTTTCCGTTCTGTACATTTT 1080
Qy 1081 GTCAAAAACCCGAAACCTTAACCTTCTGCGCGTGTACGCTCCGCTCTCTCTTCCA 1140
Db 1081 GTCAAAAACCCGAAACCTTAACCTTCTGCGCGTGTACGCTCCGCTCTCTCTTCCA 1140
Qy 1141 CATTTCAAAAGTACCCCTGTATCTCAATAATTCATCTTCACTTAACTGCTCTTTCGT 1200
Db 1141 CATTTCAAAAGTACCCCTGTATCTCAATAATTCATCTTCACTTAACTGCTCTTTCGT 1200
Qy 1201 GTGGCCTTCCACCTCCCGCAATTCGTGACGCGTACGCGACTTTGATTTATTTT 1260
Db 1201 GTGGCCTTCCACCTCCCGCAATTCGTGACGCGTACGCGACTTTGATTTATTTT 1260
Qy 1261 TTCAAAATGTTTCTCTCTACACAAACAAAGGTTCAAAAACCAAAAAA 1315
Db 1261 TTCAAAATGTTTCTCTCTACACAAACAAAGGTTCAAAAACCAAAAAA 1315

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RESULT 5
US-08-288-295-4

Sequence 4, Application US/08288295
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Hengartner, Michael
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
TITLE OF INVENTION: CELL DEATH AND USES THEREFOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A. (F) ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,295
FILING DATE: 10-AUG-1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/927,681
FILING DATE: 10-AUG-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul F.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 01997/201003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1315 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 7..846
OTHER INFORMATION: /product= "Ced-9"
US-08-288-295-4

Query Match 99.8% Score 1313; DB 6; Length 1315;
Best Local Similarity 99.9% Pred. No. 3.5e-288;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGATGACACGCTGACGCGGACAACTGCTGACGAATCCGGCGTATCGCGAGCA 60
DB 1 TTGGAGATGACACGCTGACGCGGACAACTGCTGACGAATCCGGCGTATCGCGAGCA 60
QY 61 ACGATGCGCAGCTGCGGAGATGAAGAGTTCTGGGGATATAAAGGACAGACCCACCGAT 120
DB 61 ACGATGCGCAGCTGCGGAGATGAAGAGTTCTGGGGATATAAAGGACAGACCCACCGAT 120
QY 121 TTGGATCAATAGTATGATCTCAGACTTCCATCAGCAGAGTAGGAGGCTTTCAGCGCA 180
DB 121 TTGGATCAATAGTATGATCTCAGACTTCCATCAGCAGAGTAGGAGGCTTTCAGCGCA 180
QY 181 AGAATGTCATCGAGAGTCAATTTGATGAAATCAATGATTTGGAGAGGCAAGGCTT 240
DB 181 AGAATGTCATCGAGAGTCAATTTGATGAAATCAATGATTTGGAGAGGCAAGGCTT 240
QY 241 GATATCGAGGAGTTTGTGCTGACATTTTCACGACCGAATCCGGCAAAAGCAATGGAA 300
DB 241 GATATCGAGGAGTTTGTGCTGACATTTTCACGACCGAATCCGGCAAAAGCAATGGAA 300

QY 301 TGGTTGGAGACACCGGAGATTTCGGTGTGGAGTCAACCGGACGACGAAATGATCGAGTT 360
DB 301 TGGTTGGAGACACCGGAGATTTCGGTGTGGAGTCAACCGGACGACGAAATGATCGAGTT 360
QY 361 ATGGAGACGATATTCAGAGAAAGCAACGCGGAAATTTTGGACCTCTCTGTAGACAGCTG 420
DB 361 ATGGAGACGATATTCAGAGAAAGCAACGCGGAAATTTTGGACCTCTCTGTAGACAGCTG 420
QY 421 CTCGAGTGGCCGAGATTCATTTTACGTATACAGATGTGGTGGAGCGGTTGGAAT 480
DB 421 CTCGAGTGGCCGAGATTCATTTTACGTATACAGATGTGGTGGAGCGGTTGGAAT 480
QY 481 GCACAGACGATCAATGCTCAATGTCTTATGACGTTTGTATGATCTTCTGTTGCGC 540
DB 481 GCACAGACGATCAATGCTCAATGTCTTATGACGTTTGTATGATCTTCTGTTGCGC 540
QY 541 GGTTCGTAGCTGCAAAATGATGGAATCCGTGGAACCTGAGGAGCAAGTCCGAAACCTC 600
DB 541 GGTTCGTAGCTGCAAAATGATGGAATCCGTGGAACCTGAGGAGCAAGTCCGAAACCTC 600
QY 601 TTGCTTACACATGCTGCTTATCAAAACGCGATCCGCAACACTGGAAGAACACAT 660
DB 601 TTGCTTACACATGCTGCTTATCAAAACGCGATCCGCAACACTGGAAGAACACAT 660
QY 661 CGGAGCTGGAGCACTTCATGACACTGGAACCAATGAAAGAGGACTACGAACGAGCA 720
DB 661 CGGAGCTGGAGCACTTCATGACACTGGAACCAATGAAAGAGGACTACGAACGAGCA 720
QY 721 GAACTGGAAGAGTGGAGCGCGGAGAGCAAGACAGAGGTTGATGATTTGGCGTGA 780
DB 721 GAACTGGAAGAGTGGAGCGCGGAGAGCAAGACAGAGGTTGATGATTTGGCGTGA 780
QY 781 GTAACAGCTGAGGACATTTGAATGCTTGAAGTCTGCTGTGCGCGGATGATGCTCAGC 840
DB 781 GTAACAGCTGAGGACATTTGAATGCTTGAAGTCTGCTGTGCGCGGATGATGCTCAGC 840
QY 841 TTGAAGTAACTGATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTA 900
DB 841 TTGAAGTAACTGATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTA 900
QY 901 ATCTCATTTTTCCTCACTGATCTCTCATCTCTGATCTCTGATCTCTGATCTCTGAT 960
DB 901 ATCTCATTTTTCCTCACTGATCTCTCATCTCTGATCTCTGATCTCTGATCTCTGAT 960
QY 961 CCACAAATTAACGCTCTCTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTG 1020
DB 961 CCACAAATTAACGCTCTCTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTG 1020
QY 1021 TTTTGTGGCCAAACCTCACTTCCGCTGATATCAACTTTCGCTGCTGATATTC 1080
DB 1021 TTTTGTGGCCAAACCTCACTTCCGCTGATATCAACTTTCGCTGCTGATATTC 1080
QY 1081 GTCAAAACCTCTGAACCTTAATCTTTCGCGGCTGAGCTTCCGCTCTCTGCA 1140
DB 1081 GTCAAAACCTCTGAACCTTAATCTTTCGCGGCTGAGCTTCCGCTCTCTGCA 1140
QY 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTA 1200
DB 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTA 1200
QY 1201 GTGGCCTCTTCAACTCCGCAAAATCTCTGATCGGCTAGCGACCTTGTATTAATTTT 1260
DB 1201 GTGGCCTCTTCAACTCCGCAAAATCTCTGATCGGCTAGCGACCTTGTATTAATTTT 1260
QY 1261 TTCAATTTGTTTCTCTCAACCAAAACCAAAAGCGTTCAAAAAA 1315
DB 1261 TTCAATTTGTTTCTCTCAACCAAAACCAAAAGCGTTCAAAAAA 1315

RESULT 6
US-08-288-295-5
Sequence 5, Application US/08288295

GENERAL INFORMATION:

APPLICANT: Horvitz, H. Robert
 TITLE OF INVENTION: Hengartner, Michael
 TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: FISH & RICHARDSON
 STREET: 225 Franklin Street, Suite 3100
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A. (F) ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/288,295
 FILING DATE: 10-AUG-1994
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/927,681

FILING DATE: 10-AUG-1992

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 01997/201003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1315 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

FEATURE:

NAME/KEY: CDS

LOCATION: 7..846

OTHER INFORMATION: /product= "Ccd-9"

US-08-288-295-5

Query Match

Best Local Similarity 99.8%; Score 1313; DB 6; Length 1315;
 Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTGAGATGACACGCTGCGAGCGGAGACACTCGCTGACGAATCCGGCGTATCGGCGAGCA 60
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 QY 61 ACGATGCGAGCTGCGAGATGAAGAGCTTTCTGGGATAAAGCGACAGACCCACCGAT 120
 DB 61 ACGATGCGAGCTGCGAGATGAAGAGCTTTCTGGGATAAAGCGACAGACCCACCGAT 120
 QY 121 TTTGAGATCAATAGTATGCTCAAGGAGCTTCCATCAACCGAGTAGAGGAGCTTCGACGCA 180
 DB 121 TTTGAGATCAATAGTATGCTCAAGGAGCTTCCATCAACCGAGTAGAGGAGCTTCGACGCA 180
 QY 181 AGAATGTCATCGAGAGTCAATTGATGAAAAATCAATGATGGGAGAGCCAAAGGCTT 240
 DB 181 AGAATGTCATCGAGAGTCAATTGATGAAAAATCAATGATGGGAGAGCCAAAGGCTT 240
 QY 241 GATATCGAGGATTTGGTGGCTATTTTCAGCAGCCGATCCGGCAAAACGGAATGGA 300
 DB 241 GATATCGAGGATTTGGTGGCTATTTTCAGCAGCCGATCCGGCAAAACGGAATGGA 300
 QY 301 TGGTTTGACACCGGAGTTGCGTGTGAGTAGCAACCGGACGACGAATGATGAGATT 360
 DB 301 TGGTTTGACACCGGAGTTGCGTGTGAGTAGCAACCGGACGACGAATGATGAGATT 360

DB 301 TGGTTTGACACCGGAGTTGCGTGTGAGTAGCAACCGGACGACGAATGATGAGATT 360
 QY 361 ATGGAGCGATATTCGAGAGAGAGACGCGGAAAATTTGAGACCTTGTGAGAGAGCTG 420
 DB 361 ATGGAGCGATATTCGAGAGAGAGACGCGGAAAATTTGAGACCTTGTGAGAGAGCTG 420
 QY 421 CTCGAGTGGCCAGAAATCTATTTTCTATGATGAGAGTGGTTCGAGCGTTGGAAT 480
 DB 421 CTCGAGTGGCCAGAAATCTATTTTCTATGATGAGAGTGGTTCGAGCGTTGGAAT 480
 QY 481 GCACAGACATCAATGTCATATGCTTATGACGTTTATAGCTTATCTATCTGTTGCGC 540
 DB 481 GCATAGACATCAATGTCATATGCTTATGACGTTTATAGCTTATCTATCTGTTGCGC 540
 QY 541 GGTTCGTACCTGCAAAAATGATGAGAAATCCGTGGAACCTGACGAGCAAGTGGAACTGC 600
 DB 541 GGTTCGTACCTGCAAAAATGATGAGAAATCCGTGGAACCTGACGAGCAAGTGGAACTGC 600
 QY 601 TTTGTTTACATCGCTGTTTCAATCAAAACCGGATCCGACACATGAGAGACACAT 660
 DB 601 TTTGTTTACATCGCTGTTTCAATCAAAACCGGATCCGACACATGAGAGACACAT 660
 QY 661 CGAGCTGGGAGAGCTTCAATGACACTCGGAAAACAAATGAAAGAGAGCTACGAAAGCA 720
 DB 661 CGAGCTGGGAGAGCTTCAATGACACTCGGAAAACAAATGAAAGAGAGCTACGAAAGCA 720
 QY 721 GAAGCTGAAAAAGTGGAGACCGGAGAGCAAGAACAGAGCGTGTGATGATGGCGCTGGA 780
 DB 721 GAAGCTGAAAAAGTGGAGACCGGAGAGCAAGAACAGAGCGTGTGATGATGGCGCTGGA 780
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 DB 781 GTAACGCTGGAGCCATTGGAATCCTTGAAGTGTGTTGGCGGAGATGATGTTGAGC 840
 QY 841 TTGAAGTAACTATTCATATTTGTGTAATTAATTAATTAATTAATTAATTAATTAAT 900
 DB 841 TTGAAGTAACTATTCATATTTGTGTAATTAATTAATTAATTAATTAATTAATTAAT 900
 QY 901 ATCTATTTTGGCTGACGATGATTCCTCAATCCTTGAAGTGTGTTGGCGGAGATGAT 960
 DB 901 ATCTATTTTGGCTGACGATGATTCCTCAATCCTTGAAGTGTGTTGGCGGAGATGAT 960
 QY 961 CCACAAATTTAGCGCTCTGCTGCTGATGATTAATTAATTAATTAATTAATTAATTAAT 1020
 DB 961 CCACAAATTTAGCGCTCTGCTGCTGATGATTAATTAATTAATTAATTAATTAATTAAT 1020
 QY 1021 TTTTGTGTCGCAAAACCTTACCTTCCGCTAATATCAACTTTTCCGCTGATGATGAT 1080
 DB 1021 TTTTGTGTCGCAAAACCTTACCTTCCGCTAATATCAACTTTTCCGCTGATGATGAT 1080
 QY 1081 GTCAAAAACCTGAAACCTTATCTTCTGCGGCTGATGATGATGATGATGATGATGAT 1140
 DB 1081 GTCAAAAACCTGAAACCTTATCTTCTGCGGCTGATGATGATGATGATGATGATGAT 1140
 QY 1141 CATTTCCAAAGTACCCCTGATCTCAATATTAATTAATTAATTAATTAATTAATTAAT 1200
 DB 1141 CATTTCCAAAGTACCCCTGATCTCAATATTAATTAATTAATTAATTAATTAATTAAT 1200
 QY 1201 GTGGCTCTTCCAAACCTTCCGCTGATGATGATGATGATGATGATGATGATGATGAT 1260
 DB 1201 GTGGCTCTTCCAAACCTTCCGCTGATGATGATGATGATGATGATGATGATGATGAT 1260
 QY 1261 TTCAAAATTTTCTCTCTACACACAAACAAACAAACAAACAAACAAACAAACAAACAA 1315
 DB 1261 TTCAAAATTTTCTCTCTACACACAAACAAACAAACAAACAAACAAACAAACAAACAA 1315

RESULT 7

US-08-288-295-6

; Sequence 6, Application US/08288295

; GENERAL INFORMATION:

; APPLICANT: Horvitz, H. Robert

; APPLICANT: Hengartner, Michael

TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
 TITLE OF INVENTION: CELL DEATH AND USES THEREFOR
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: FISH & RICHARDSON
 STREET: 225 Franklin Street, Suite 3100
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A. (F) ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.0
 CURRENT APPLICATION DATA: US/08/288,295
 APPLICATION NUMBER: US/08/288,295
 FILING DATE: 10-AUG-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/927,681
 FILING DATE: 10-AUG-1992
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 01997/201003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1315 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..846
 OTHER INFORMATION: /product= "Ced-9"
 US-08-288-295-6

Query Match 99.8%; Score 1313; DB 6; Length 1315;
 Best Local Similarity 99.9%; Pred. No. 3.5e-288;
 Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 361 ATGGGACGATTTTGAGAGAGAGACGCGGAAATTTTGAGACTTCTGTGAGAGAGCTG 420
 421 CTGCGAGTCCCGAGAGATTCATTTTACTGTATTCAGAGATGCGTTCGAGCGGTGGAAT 480
 422 CTGCGAGTCCCGAGAGATTCATTTTACTGTATTCAGAGATGCGTTCGAGCGGTGGAAT 480
 481 GCACAGACAGATCAATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 540
 481 GCACAGACAGATCAATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 540
 541 GATTTCGAGTCCCGAGAGATTCATTTTACTGTATTCAGAGATGCGTTCGAGCGGTGGAAT 600
 541 GATTTCGAGTCCCGAGAGATTCATTTTACTGTATTCAGAGATGCGTTCGAGCGGTGGAAT 600
 601 TTGCTTTACACATCGCTGTTTCATCAAAAGCGGATCCGACAACTGGAAGAGACAAAT 660
 601 TTGCTTTACACATCGCTGTTTCATCAAAAGCGGATCCGACAACTGGAAGAGACAAAT 660
 661 CGGAGCTGGAGCAGCTTCATGACACTCGGAAACAAATGAAAGAGACTACGAAAGAGCA 720
 661 CGGAGCTGGAGCAGCTTCATGACACTCGGAAACAAATGAAAGAGACTACGAAAGAGCA 720
 721 GAACCTGAAAGAGTGGAGACCGCGGAAAGCAGACAGAGCGTGTGATGATGCGCTGGA 780
 721 GAACCTGAAAGAGTGGAGACCGCGGAAAGCAGACAGAGCGTGTGATGATGCGCTGGA 780
 781 GTACAGCTGGAGCAGCTTCATGACACTCGGAAACAAATGAAAGAGACTACGAAAGAGCA 840
 781 GTACAGCTGGAGCAGCTTCATGACACTCGGAAACAAATGAAAGAGACTACGAAAGAGCA 840
 841 TTGAAGTACGATTCATTTTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
 841 TTGAAGTACGATTCATTTTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
 901 ATCTCATTTTGTCTCAGTATTCATTTTGTATTAATTAATTAATTAATTAATTAATTAAT 960
 901 ATCTCATTTTGTCTCAGTATTCATTTTGTATTAATTAATTAATTAATTAATTAATTAAT 960
 961 CCACAAATTTAGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 961 CCACAAATTTAGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 1021 TTTTTCGCGCAAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 1021 TTTTTCGCGCAAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
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 1141 CATTTCCAAAGTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 1141 CATTTCCAAAGTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 1201 GTGGCTCTTCCAAAGTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
 1201 GTGGCTCTTCCAAAGTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
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 1261 TTCAAAATGTTTCTCTCTACCAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAA 1315

RESULT 8
 US-08-801-248-4
 Sequence 4, Application US/08801248
 GENERAL INFORMATION:
 APPLICANT: Horvitz, H. Robert
 APPLICANT: Hengartner, Michael
 TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
 TITLE OF INVENTION: CELL DEATH AND USES THEREFOR


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: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FISH & RICHARDSON
: STREET: 225 Franklin Street, Suite 3100
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Wordperfect 5.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/801,248
: FILING DATE: 19-FEB-1997
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/288,295
: FILING DATE: 10-AUG-1994
: APPLICATION NUMBER: US 07/927,681
: FILING DATE: 10-AUG-1992
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,162
: REFERENCE/DOCKET NUMBER: 01997/201003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-5070
: TELEFAX: (617) 542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1315 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 7..846
: OTHER INFORMATION: /product= "Ced-9"
: US-08-801-248-4

Query Match      99.8%; Score 1313; DB 12; Length 1315;
Best Local Similarity 99.9%; Pred. No. 3,5e-288;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      361 ATGGGACGATATTCGAGAAAGACGCGGAAATTTGAGACCTTCTGACACTG 420
      421 CTCGAGTGGCCAGATCTCATTTTCACTGATACAGATGTGGTTCGAGCGTTGAAAT 480
      422 CTCGAGTGGCCAGATCTCATTTTCACTGATACAGATGTGGTTCGAGCGTTGAAAT 480
      481 GCACAGACAGATCATGTCTATGCTATGAGAGCTTGAAGCTTAATCTGCTGGC 540
      481 GCACAGACAGATCATGTCTATGCTATGAGAGCTTGAAGCTTGAATCTGCTGGC 540
      541 GGTTCGTAAGCTGCAAAAATGATGAAATCCGTGAACTGACAGGCAAGTCCGAACTC 600
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      661 CGAGCTGGGACGACTTCATGACACTCGGAAACAAATGAAAGAGACTACGAACGACA 720
      661 CGAGCTGGGACGACTTCATGACACTCGGAAACAAATGAAAGAGACTACGAACGACA 720
      721 GAAGCTGAAAAAGTGGGACCGCGGAACACAGACAGCGTGTGATGATTCGCTGGA 780
      721 GAAGCTGAAAAAGTGGGACCGCGGAACACAGACAGCGTGTGATGATTCGCTGGA 780
      781 GTAACAGCTGGAGCCATTTGAATGCTGGAGTGTGCTGTGGGGAGATGTTCCAG 840
      781 GTAACAGCTGGAGCCATTTGAATGCTGGAGTGTGCTGTGGGGAGATGTTCCAG 840
      841 TTGAAGTAAAGCTATTCATTTTGTAAATTAATTAATTAATTAATTAATTAATTA 900
      901 ATCTATTTTGGCTCACTGATTCCTCATCCTTGAAGTGAAGTGAAGTGAAGTGAAG 960
      901 ATCTATTTTGGCTCACTGATTCCTCATCCTTGAAGTGAAGTGAAGTGAAGTGAAG 960
      961 CCACAAATTAAGGCTCTGCTGTGATGATTAAGATTAAGATTAAGATTAAGATTAAG 1020
      961 CCACAAATTAAGGCTCTGCTGTGATGATTAAGATTAAGATTAAGATTAAGATTAAG 1020
      1021 TTTTGTGGGCAACCCCTACTTCCGCGTAAATATCAACTTTTCCGTTCTGTACATTT 1080
      1021 TTTTGTGGGCAACCCCTACTTCCGCGTAAATATCAACTTTTCCGTTCTGTACATTT 1080
      1081 GTCAAAACCCCTGAAACCCCTACTTTCGCGTGAAGTGAAGTGAAGTGAAGTGAAG 1140
      1081 GTCAAAACCCCTGAAACCCCTACTTTCGCGTGAAGTGAAGTGAAGTGAAGTGAAG 1140
      1141 CATTTCGAAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTA 1200
      1141 CATTTCGAAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTA 1200
      1201 GTGGCCTCTTCAACCTCCCAAAATCTCTGACGAGTGAAGGAGCTTGAATTTT 1260
      1201 GTGGCCTCTTCAACCTCCCAAAATCTCTGACGAGTGAAGGAGCTTGAATTTT 1260
      1261 TTCAATTTTCTCTCTACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1315
      1261 TTCAATTTTCTCTCTACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1315

RESULT 9
US-08-801-248-5
: Sequence 5, Application US/08801248
: GENERAL INFORMATION:
: APPLICANT: Horvitz, H. Robert
: APPLICANT: Hengartner, Michael
: TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
: TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
: TITLE OF INVENTION: CELL DEATH AND USES THEREFOR

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NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & RICHARDSON
 STREET: 225 Franklin Street, Suite 3100
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,248
 FILING DATE: 19-FEB-1997
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/288,295
 FILING DATE: 10-AUG-1994
 APPLICATION NUMBER: US 07/927,681
 FILING DATE: 10-AUG-1992
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 01997/201003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ. ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1315 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..846
 OTHER INFORMATION: /product= "Ced-9"
 US-08-801-248-5

Query Match 99.8%; Score 1313; DB 12; Length 1315;
 Best Local Similarity 99.9%; Pred. No. 3.5e-288;
 Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 TTTGAGATGACACGCTGACGCGGAGACACTGCTGACGAAATCCGGCGTATGCGGCGACGA 60
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DB 61 ACGATGGCGACTGGCGAGATGAAAGAGTTCTGCGGATTAAGGACAGAGCCACCGAT 120
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DB 121 TTTGGAATCAATAGATGATGCTCAGAGCTTGCCATCACCAGATGAGAGGCTTGACGCGA 180
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DB 121 TTTGGAATCAATAGATGATGCTCAGAGCTTGCCATCACCAGATGAGAGGCTTGACGCGA 180
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DB 361 ATGGAGCAGATTTTGCAGAGAGACCGCGGAAATTTTGAACCTTCTGTGAGACAGCTG 420
OY 421 CTCGACGTGCCCGAATCTCATATTTTACGTATACAGATGTGTTGGACGGTTGGAAT 480
DB 421 CTCGACGTGCCCGAATCTCATATTTTACGTATACAGATGTGTTGGACGGTTGGAAT 480
OY 481 GCACAGACAGATCAATGTCATGCTTATGAGACGTTTGTATGATCTTCTGTGGC 540
DB 481 GCATAGACAGATCAATGTCATGCTTATGAGACGTTTGTATGATCTTCTGTGGC 540
OY 541 GGTTCGTACCTGCAAAATGATGGAATCCGTGGAATCGAGGACAAAGTGGCAACCTC 600
DB 541 GGTTCGTACCTGCAAAATGATGGAATCCGTGGAATCGAGGACAAAGTGGCAACCTC 600
OY 601 TTGCTTTACATCGCTGTTTATCAAAACCGGATCCGCAACAACTGGAAGAACCAAT 660
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OY 841 TTGAAGTACGATTCATTAATTTGTGTAATTAATTAATTAATTAATTAATTAATTA 900
DB 841 TTGAAGTACGATTCATTAATTTGTGTAATTAATTAATTAATTAATTAATTAATTA 900
OY 901 ATCTATTTTGGCTACGATGATCTCTCATCTTGAACCTGGAAGAGTGGAAAGCTAGG 960
DB 901 ATCTATTTTGGCTACGATGATCTCTCATCTTGAACCTGGAAGAGTGGAAAGCTAGG 960
OY 961 CCACAAATTAAGGCTCTGCTGTGATTTAGATTTTACTGCAATTTTTCGATTGCT 1020
DB 961 CCACAAATTAAGGCTCTGCTGTGATTTAGATTTTACTGCAATTTTTCGATTGCT 1020
OY 1021 TTTTGTGGGCAAAACCTCTACTTCGCGTAATATCAATTTTCCGTGTTCTGATTTTC 1080
DB 1021 TTTTGTGGGCAAAACCTCTACTTCGCGTAATATCAATTTTCCGTGTTCTGATTTTC 1080
OY 1081 GTCAAAACCTGAAACCTTAATTTCTGCGCGTGAAGCTTCCGCTTCTTCCA 1140
DB 1081 GTCAAAACCTGAAACCTTAATTTCTGCGCGTGAAGCTTCCGCTTCTTCCA 1140
OY 1141 CATTTCCAAAGTACCCCTGTATCTCAATTAATTCATTTTCACTTTAAGTCTCTTTGCT 1200
DB 1141 CATTTCCAAAGTACCCCTGTATCTCAATTAATTCATTTTCACTTTAAGTCTCTTTGCT 1200
OY 1201 GTGGCCTCTTCAACCTCCCGCAAAATTCCTGACGAGTACGAGGACTTTGATTTT 1260
DB 1201 GTGGCCTCTTCAACCTCCCGCAAAATTCCTGACGAGTACGAGGACTTTGATTTT 1260
OY 1261 TTCAAAATGTTTCTCTTCAACCAACAAAAAAGGTTCAAAAAA 1315
DB 1261 TTCAAAATGTTTCTCTTCAACCAACAAAAAAGGTTCAAAAAA 1315
  
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RESULT 10
 US-08-801-248-6
 ; Sequence 6, Application US/08801248
 ; GENERAL INFORMATION:
 ; APPLICANT: Horvitz, H. Robert
 ; APPLICANT: Hengartner, Michael
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 ; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
 ; TITLE OF INVENTION: CELL DEATH AND USES THEREFOR

```

? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: FISH & RICHARDSON
? STREET: 225 Franklin Street, Suite 3100
? CITY: Boston
? STATE: Massachusetts
? COUNTRY: U.S.A.
? ZIP: 02110-2804
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Nordperfect 5.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/801,248
? FILING DATE: 19-FEB-1997
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/288,295
? FILING DATE: 10-AUG-1994
? APPLICATION NUMBER: US 07/927,681
? FILING DATE: 10-AUG-1992
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Clark, Paul T.
? REGISTRATION NUMBER: 30,162
? REFERENCE/DOCKET NUMBER: 01997/201003
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617) 542-5070
? TELEFAX: (617) 542-8906
? TELEX: 200154
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1315 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 7..846
? OTHER INFORMATION: /product="Ced-9"
? US-08-801-248-6

```

Query Match 99.8%; Score 1313; DB 12; Length 1315;
 Best Local Similarity 99.98; Fred. No. 3.5e-288;
 Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 TTGAGATGACACGCTGCACGCGGACAACTGCTGACGAATCCGGCGGTATCGGCGACGA 60
DB 1 TTGAGATGACACGCTGCACGCGGACAACTGCTGACGAATCCGGCGGTATCGGCGACGA 60
QY 61 ACGATGGGACTGCGGAGATGAGAGAGTTCTGCGGATTAAGGACACAGACCCACCGAT 120
DB 61 ACGATGGGACTGCGGAGATGAGAGAGTTCTGCGGATTAAGGACACAGACCCACCGAT 120
QY 121 TTGGAATCAATAGTATGATGCTCAGGACTTGCATACCGAGATAGGAGGCTTCACGCGA 180
DB 121 TTGGAATCAATAGTATGATGCTCAGGACTTGCATACCGAGATAGGAGGCTTCACGCGA 180
QY 181 AGAATGTCATCGAGAGTCAATTGATGAGAAAAATCAATGATGATGGAAGAGCCAAAGCTT 240
DB 181 AGAATGTCATCGAGAGTCAATTGATGAGAAAAATCAATGATGATGGAAGAGCCAAAGCTT 240
QY 241 GATATCGAGGATTTGGTGTGCTGACTATTTCACGACCGAATCCGGCAAAACGGAATGAA 300
DB 241 GATATCGAGGATTTGGTGTGCTGACTATTTCACGACCGAATCCGGCAAAACGGAATGAA 300
QY 301 TGGTTTGAGACCGGCGGATTCCTGTGAGATGCAACCGGAGCAAGAAATGATCGCGATT 360
DB 301 TGGTTTGAGACCGGCGGATTCCTGTGAGATGCAACCGGAGCAAGAAATGATCGCGATT 360
QY 361 ATGGGAACGATATTTCGAAAGAAAGACACGCGGAAAAATTTTGAAGACCTTCTGTGACAGCTG 420

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DB 361 ATGGGAACGATATTCGAGAAGAACACGCGGAAAAATTTTGAAGACCTTCTGTGACAGCTG 420
QY 421 CTCGCGATGCCGAGAAATCTCATTTTACCTGATATCGAGATGTGTTGGACGGTTGGAAT 480
DB 421 CTCGCGATGCCGAGAAATCTCATTTTACCTGATATCGAGATGTGTTGGACGGTTGGAAT 480
QY 481 GCACAGACAGATCAATGTCATATGCTTATGAGACCTTTGATAGTCTATCTCGTTGGC 540
DB 481 GCACAGACAGATCAATGTCATATGCTTATGAGACCTTTGATAGTCTATCTCGTTGGC 540
QY 541 GGTTCGTAGCTGCAAAAAATGATGAAATCCGTGGAATCTGACAGGACAAAGTCCGAAACCTC 600
DB 541 GGTTCGTAGCTGCAAAAAATGATGAAATCCGTGGAATCCGTGGAATCTGACAGGACAAAGTCC 600
QY 601 TTCGTTTACATTCGCTGTTTCATCAAAACGGGAGATCCGCAACATCGGAAGACACAAAT 660
DB 601 TTCGTTTACATTCGCTGTTTCATCAAAACGGGAGATCCGCAACATCGGAAGACACAAAT 660
QY 661 CGGAGCTGGAGACGACTTATGACACTCGGAAACAAATGAAAGAGACTACGACGACGA 720
DB 661 CGGAGCTGGAGACGACTTATGACACTCGGAAACAAATGAAAGAGACTACGACGACGA 720
QY 721 GAAGCTGAAAAAGTGGGACGCGGAGAGACAGACGAGGTGATGATTTGCGCTGGA 780
DB 721 GAAGCTGAAAAAGTGGGACGCGGAGAGACAGACGAGGTGATGATTTGCGCTGGA 780
QY 781 GTAAACGCTGAGACCATTTGGAATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 GTAAACGCTGAGACCATTTGGAATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 TTGAAGTACGATATTCATTTTGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
DB 841 TTGAAGTACGATATTCATTTTGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
QY 901 ATCTCATTTTTCGCTCAGTATTCCTCATCCTTGAACGAGAGAGTGGGAAAGCTAGG 960
DB 901 ATCTCATTTTTCGCTCAGTATTCCTCATCCTTGAACGAGAGAGTGGGAAAGCTAGG 960
QY 961 CCACAAATTCAGGCTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 961 CCACAAATTCAGGCTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 TTTTTCGCAAAACCTTCTCCGCTGATATTCATCTTTCCGTTCTGTACATTTTC 1080
DB 1021 TTTTTCGCAAAACCTTCTCCGCTGATATTCATCTTTCCGTTCTGTACATTTTC 1080
QY 1081 GTCAAAAACCTTGAACCTTAATTTTCGCGGAGCTAGGCTCCGCTTCTCTTCCA 1140
DB 1081 GTCAAAAACCTTGAACCTTAATTTTCGCGGAGCTAGGCTCCGCTTCTCTTCCA 1140
QY 1141 CATTTCCAAAGTAAACCTTCTGATATTCATTAATTAATTAATTAATTAATTAATTAATTA 1200
DB 1141 CATTTCCAAAGTAAACCTTCTGATATTCATTAATTAATTAATTAATTAATTAATTAATTA 1200
QY 1201 GTGGCCTCTTCCAACTCCGCAAAATTCCTGATGAGGCTAGGAGCTTGTATTTATTTT 1260
DB 1201 GTGGCCTCTTCCAACTCCGCAAAATTCCTGATGAGGCTAGGAGCTTGTATTTATTTT 1260
QY 1261 TTTCAATTTGTTTCTGTACAAACAACAAAAAAGTTTCAAAAAAAGTTTCAAAAAAAGTTT 1315
DB 1261 TTTCAATTTGTTTCTGTACAAACAACAAAAAAGTTTCAAAAAAAGTTTCAAAAAAAGTTT 1315

```

RESULT 11
 US-09-993-420A-4
 ; Sequence 4, Application US/09993420A
 ; GENERAL INFORMATION:
 ; APPLICANT: Horvitz, H. Robert
 ; APPLICANT: Hengartner, Michael
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 ; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
 ; TITLE OF INVENTION: USES THEREOF

```

FILE REFERENCE: 01997/201006
CURRENT APPLICATION NUMBER: US/09/993,420A
CURRENT FILING DATE: 5001-11-09
PRIOR APPLICATION NUMBER: 09/234,186
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: 07/898,933
PRIOR FILING DATE: 1992-06-12
PRIOR APPLICATION NUMBER: 07/927,681
PRIOR FILING DATE: 1992-08-10
PRIOR APPLICATION NUMBER: 08/288,295
PRIOR FILING DATE: 1994-08-10
PRIOR APPLICATION NUMBER: 08/801,248
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1315
TYPE: DNA
ORGANISM: Caenorhabditis elegans
FEATURE:
NAME/KEY: CDS
LOCATION: (77)...(846)
US-09-993-420A-4

```

```

Query Match          99.8%; Score 1313; DB 37; Length 1315;
Best Local Similarity 99.9%; Pred. No. 3.5e-288;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 TTTGAGATGACACGCTCCACGCGGACACACTCGCTGACGATCCGGCGTTCGGCGACGA 60
DB 1 TTTGAGATGACACGCTCCACGCGGACACACTCGCTGACGATCCGGCGTTCGGCGACGA 60
QY 61 ACGATGCGACGCTGCGAGATCAAGAGTTCCTGGGATAAAGGACACAGAGCCACCGAT 120
DB 61 ACGATGCGACGCTGCGAGATCAAGAGTTCCTGGGATAAAGGACACAGAGCCACCGAT 120
QY 121 TTTGGAATCAATAGTGTGCTCAGAGCTTGGCCATCACCGAGTAGGAGGCTTCGACGCGA 180
DB 121 TTTGGAATCAATAGTGTGCTCAGAGCTTGGCCATCACCGAGTAGGAGGCTTCGACGCGA 180
QY 121 TTTGGAATCAATAGTGTGCTCAGAGCTTGGCCATCACCGAGTAGGAGGCTTCGACGCGA 180
DB 121 TTTGGAATCAATAGTGTGCTCAGAGCTTGGCCATCACCGAGTAGGAGGCTTCGACGCGA 180
QY 181 AGAATGTCATCGAGAGTCAATGATGGAATAATCAATGATTTGGGAAGAGCCAAAGCTT 240
DB 181 AGAATGTCATCGAGAGTCAATGATGGAATAATCAATGATTTGGGAAGAGCCAAAGCTT 240
QY 241 GATATCGAGGAGTTGGTGACATTTTCACGACCGAATCCCGCAAAACGGAATGGA 300
DB 241 GATATCGAGGAGTTGGTGACATTTTCACGACCGAATCCCGCAAAACGGAATGGA 300
QY 301 TGGTTTGAGAGCAGCGGATTCGCTGTGAGTGCACACCGAGACAGGAATGATCGAGTT 360
DB 301 TGGTTTGAGAGCAGCGGATTCGCTGTGAGTGCACACCGAGAGCAAGATGATCGAGTT 360
QY 361 ATGGAGACGATTTGAGAGAGAGACCGGAAAAATTTTGAGACCTTGTGAGAGAGCTG 420
DB 361 ATGGAGACGATTTGAGAGAGAGACCGGAAAAATTTTGAGACCTTGTGAGAGAGCTG 420
QY 421 CTGCGAGTCCGAGATTCATTTTCATGATCAGATGATGATGATGATGATGATGATGAT 480
DB 421 CTGCGAGTCCGAGATTCATTTTCATGATCAGATGATGATGATGATGATGATGATGAT 480
QY 481 GCACAGACGATCAATGTCATGCTTATGAGAGCTTTGATGATGATGATGATGATGATGAT 540
DB 481 GCACAGACGATCAATGTCATGCTTATGAGAGCTTTGATGATGATGATGATGATGATGAT 540
QY 541 GGTTCGTGAGTGCAGAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 GGTTCGTGAGTGCAGAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 TTTGTTTACATGCTGCTTTCATCAAAACGCGATCCGACAACTGGAAGAGACATAT 660
DB 601 TTTGTTTACATGCTGCTTTCATCAAAACGCGATCCGACAACTGGAAGAGACATAT 660
QY 661 CGAGAGCTGGAGACTTTCATGACACTCGGAAAAAATGAAGAGATACGACAGAGCA 720

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DB 661 CGAGAGCTGGAGACTTTCATGACACTCGGAAAAAATGAAGAGATACGACAGAGCA 720
QY 721 GAAGCTGAAAAATGAGGAGCGCGGAGACAGACAGAGAGGTCGATGATGCGCTGGA 780
DB 721 GAAGCTGAAAAATGAGGAGCGCGGAGACAGACAGAGAGGTCGATGATGCGCTGGA 780
QY 781 GTAACAGCTGAGGACATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 GTAACAGCTGAGGACATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 TTTGAGTACGATTTCAATTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 TTTGAGTACGATTTCAATTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 ATTCATTTTGGCTCAGATTTCTCATTCCTTTGAACCTGAGAGAGTGGGAAAGCTAGG 960
DB 901 ATTCATTTTGGCTCAGATTTCTCATTCCTTTGAACCTGAGAGAGTGGGAAAGCTAGG 960
QY 961 CCACAATTTAGGCTCTCTGTGTGATTTAGCATTTTACTGCAATTTTCCGATGCT 1020
DB 961 CCACAATTTAGGCTCTCTGTGTGATTTAGCATTTTACTGCAATTTTCCGATGCT 1020
QY 1021 TTTTGTGGCCAAACCTCTCTGTGTGATTTAGCATTTTACTGCAATTTTCCGATGCT 1080
DB 1021 TTTTGTGGCCAAACCTCTCTGTGTGATTTAGCATTTTACTGCAATTTTCCGATGCT 1080
QY 1081 GTCAAAAACCCCTGAACCCCTTAATTTTCTGCGGCTGAGCTCCGCTTCCTTCCA 1140
DB 1081 GTCAAAAACCCCTGAACCCCTTAATTTTCTGCGGCTGAGCTCCGCTTCCTTCCA 1140
QY 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
DB 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
QY 1201 GTGGCCTCTTCCACCTCCCGCAATTCCTGAGCGATGAGGACTTTGATTTATTTT 1260
DB 1201 GTGGCCTCTTCCACCTCCCGCAATTCCTGAGCGATGAGGACTTTGATTTATTTT 1260
QY 1261 TTTCAATTTGTTTCTCTCTACAAACAACAAAAACGTTCAAAAAA 1315
DB 1261 TTTCAATTTGTTTCTCTCTACAAACAACAAAAACGTTCAAAAAA 1315

RESULT 12
US-09-993-420A-5
; Sequence 5, Application US/09993420A
; GENERAL INFORMATION:
; APPLICANT: Hengartner, H. Robert
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 01997/201006
; CURRENT APPLICATION NUMBER: US/09/993,420A
; CURRENT FILING DATE: 5001-11-09
; PRIOR APPLICATION NUMBER: 09/234,186
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:

```

NAME/KEY: CDS
LOCATION: (77)...(846)
US-09-993-420a-5

Query Match 99.8%; Score 1313; DB 37; Length 1315;
Best Local Similarity 99.9%; Pred. No. 3.5e-288;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 TTTGAGATGACAGCTGACGAGGAGCAACTGCTGACGAATCGGCGATATGCGGACGCA 60
DB 1 TTTGAGATGACAGCTGACGAGGAGCAACTGCTGACGAATCGGCGATATGCGGACGCA 60
QY 61 ACATGCGGAGCTGCGGAGATGAGAGAGTTCTGGGATAAAGGACAGAGCCACCGAT 120
DB 61 ACATGCGGAGCTGCGGAGATGAGAGAGTTCTGGGATAAAGGACAGAGCCACCGAT 120
QY 121 TTTGGAATCAATAGTATGCTCAGGACTGCTGACGATCCACCGATGAGAGCTTCGACGCA 180
DB 121 TTTGGAATCAATAGTATGCTCAGGACTGCTGACGATCCACCGATGAGAGCTTCGACGCA 180
QY 181 AGAATGTCATCGAGAGATCAATTTGATGAAAAATCAATGATTTGGGAGGCGACGCTT 240
DB 181 AGAATGTCATCGAGAGATCAATTTGATGAAAAATCAATGATTTGGGAGGCGACGCTT 240
QY 241 GATATGAGGAGATTTGTGCTGACTATTTTCAGCACCGAATCCGGCAAAACGGAATGGA 300
DB 241 GATATGAGGAGATTTGTGCTGACTATTTTCAGCACCGAATCCGGCAAAACGGAATGGA 300
QY 301 TGGTTTGAGACACCGGAGATTCGCTGAGAGCAACCGGACGAGAAATGATGCGAGTT 360
DB 301 TGGTTTGAGACACCGGAGATTCGCTGAGAGCAACCGGACGAGAAATGATGCGAGTT 360
QY 361 ATGGGACATATTCGAGAGAGACACCGGAAATTTTGAAGACCTTCGTGACGACGTG 420
DB 361 ATGGGACATATTCGAGAGAGACACCGGAAATTTTGAAGACCTTCGTGACGACGTG 420
QY 421 CTCGCGATCCGAGATTCATTTTCACTGATTCAGAGATGCTGTCGAGCGGTTGGAAT 480
DB 421 CTCGCGATCCGAGATTCATTTTCACTGATTCAGAGATGCTGTCGAGCGGTTGGAAT 480
QY 481 GCAGACAGACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 540
DB 481 GCAGACAGACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 540
QY 541 GGTTCGTAAGCTGCAAAAATGATGGAATCCGTAAGTGCAGAGGACAGTAGTGGAAACCTC 600
DB 541 GGTTCGTAAGCTGCAAAAATGATGGAATCCGTAAGTGCAGAGGACAGTAGTGGAAACCTC 600
QY 601 TTCGTTTACATTCGCTGTCATCAAAAACGGGATCCGCAACCACTGAGAACACAT 660
DB 601 TTCGTTTACATTCGCTGTCATCAAAAACGGGATCCGCAACCACTGAGAACACAT 660
QY 661 CGGAGCTGGAGAGCTTCATGACACTCGGAAACAAATGAAGAGACTAGAGAGAGCA 720
DB 661 CGGAGCTGGAGAGCTTCATGACACTCGGAAACAAATGAAGAGACTAGAGAGAGCA 720
QY 721 GAAGCTGAAAAAGTGGGAGCGCGAGAGCAAGACAGAGCTGTGATGATTTGGCGTGA 780
DB 721 GAAGCTGAAAAAGTGGGAGCGCGAGAGCAAGACAGAGCTGTGATGATTTGGCGTGA 780
QY 781 GTAAACAGTGAAGCATTTGGAATGCTGAGATGCTGAGGCGGAGATGATTTGAGC 840
DB 781 GTAAACAGTGAAGCATTTGGAATGCTGAGATGCTGAGGCGGAGATGATTTGAGC 840
QY 841 TTGAAGTACGATTTCAATTTGTAAATTAATTAATTAATTAATTAATTAATTAATTTGA 900
DB 841 TTGAAGTACGATTTCAATTTGTAAATTAATTAATTAATTAATTAATTAATTTGA 900
QY 901 ATTCATTTTGTGACGATTTCTGATCTTGAATGAGAGAGTGGGAAAGCTAGG 960
DB 901 ATTCATTTTGTGACGATTTCTGATCTTGAATGAGAGAGTGGGAAAGCTAGG 960
QY 961 CCACAATTTACGCTCTCTGTGATTTAGATTTTACTGCAATTTTTCGATTCCT 1020

```

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DB 961 CCACAATTTACGCTCTCTGTGATTTAGATTTTACTGCAATTTTTCGATTCCT 1020
QY 1021 TTTTGTGGCCAAACCTTACTTCCGTAATATACCTTTCCGTGTCATCTTC 1080
DB 1021 TTTTGTGGCCAAACCTTACTTCCGTAATATACCTTTCCGTGTCATCTTC 1080
QY 1081 GTCAAAAACCTGAAACCTTAATTTCTGCGCGGTAGCCCTCCGCTTCCTTCA 1140
DB 1081 GTCAAAAACCTGAAACCTTAATTTCTGCGCGGTAGCCCTCCGCTTCCTTCA 1140
QY 1141 CATTTCCAAAGTACCCCGTATCTCAATTAATTAATTAATTAATTAATTTTCT 1200
DB 1141 CATTTCCAAAGTACCCCGTATCTCAATTAATTAATTAATTAATTTTCT 1200
QY 1201 GTGGCCTTCCAACTCCCGCAATTCCTGACGAGTACGAGCTTGTATTTT 1260
DB 1201 GTGGCCTTCCAACTCCCGCAATTCCTGACGAGTACGAGCTTGTATTTT 1260
QY 1261 TTCAATTTGTTCTCTCTTACACACAAAAAAGGTTCAAAAAA 1315
DB 1261 TTCAATTTGTTCTCTCTTACACACAAAAAAGGTTCAAAAAA 1315

```

RESULT 13

US-09-993-420a-6

Sequence 6, Application US/0993420A

GENERAL INFORMATION:

APPLICANT: Horvitz, H. Robert

APPLICANT: Hengartner, Michael

TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A

TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND

FILE REFERENCE: US97/201006

CURRENT APPLICATION NUMBER: US/09/993,420A

PRIOR FILING DATE: 5001-11-09

PRIOR APPLICATION NUMBER: 09/234,186

PRIOR FILING DATE: 1999-01-20

PRIOR APPLICATION NUMBER: 07/898,933

PRIOR FILING DATE: 1992-06-12

PRIOR APPLICATION NUMBER: 07/927,681

PRIOR FILING DATE: 1992-08-10

PRIOR APPLICATION NUMBER: 08/288,295

PRIOR FILING DATE: 1994-08-10

PRIOR APPLICATION NUMBER: 08/801,248

PRIOR FILING DATE: 1997-02-19

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 1315

TYPE: DNA

ORGANISM: Caenorhabditis elegans

FEATURE:

NAME/KEY: CDS

LOCATION: (77)...(846)

US-09-993-420a-6

Query Match 99.8%; Score 1313; DB 37; Length 1315;
Best Local Similarity 99.9%; Pred. No. 3.5e-288;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 TTTGAGATGACAGCTGACGAGGAGCAACTGCTGACGAATCCGCGATATGCGGACGCA 60
DB 1 TTTGAGATGACAGCTGACGAGGAGCAACTGCTGACGAATCCGCGATATGCGGACGCA 60
QY 61 ACATGCGGAGCTGCGGAGATGAGAGAGTTCTGGGATAAAGGACAGAGCCACCGAT 120
DB 61 ACATGCGGAGCTGCGGAGATGAGAGAGTTCTGGGATAAAGGACAGAGCCACCGAT 120
QY 121 TTTGGAATCAATAGTATGCTCAGGACTGCTGACGATCCACCGATGAGAGCTTCGACGCA 180
DB 121 TTTGGAATCAATAGTATGCTCAGGACTGCTGACGATCCACCGATGAGAGCTTCGACGCA 180

```

QY 181 AGAATGTCATCGAGAGTCATTTGATGAAAAATCATGATTGGAGAGCCAGGCTT 240
 181 AGAATGTCATCGAGAGTCATTTGATGAAAAATCATGATTGGAGAGCCAGGCTT 240
 QY 241 GATATGAGGAGTATTTGGTGCAGTATTTACAGCAGCAGATCCGGAAAAAGGATGAA 300
 241 GATATGAGGAGTATTTGGTGCAGTATTTACAGCAGCAGATCCGGAAAAAGGATGAA 300
 Db 241 GATATGAGGAGTATTTGGTGCAGTATTTACAGCAGCAGATCCGGAAAAAGGATGAA 300
 QY 301 TGGTTGGAGCACCAGGAGTCCGTGTGAGTCAACCGAGACGCAAAATGATGCGAGTT 360
 301 TGGTTGGAGCACCAGGAGTCCGTGTGAGTCAACCGAGACGCAAAATGATGCGAGTT 360
 Db 301 TGGTTGGAGCACCAGGAGTCCGTGTGAGTCAACCGAGACGCAAAATGATGCGAGTT 360
 QY 361 ATGGGAACGATTTTCGAGAAAGACGACGCGGAAAAATTTTGAACCTTCTGTGAGCAGCTG 420
 361 ATGGGAACGATTTTCGAGAAAGACGACGCGGAAAAATTTTGAACCTTCTGTGAGCAGCTG 420
 Db 361 ATGGGAACGATTTTCGAGAAAGACGACGCGGAAAAATTTTGAACCTTCTGTGAGCAGCTG 420
 QY 421 CTGCGAGTGGCCAGAAATCTATTTTCATCTGATCAGAGTGTGTTGGAGGAT 480
 421 CTGCGAGTGGCCAGAAATCTATTTTCATCTGATCAGAGTGTGTTGGAGGAT 480
 Db 421 CTGCGAGTGGCCAGAAATCTATTTTCATCTGATCAGAGTGTGTTGGAGGAT 480
 QY 481 GCACAGACAGATCAATGTCCATGTCTTATGAGCGTTTATGAGTCTATCTGTTGGC 540
 481 GCACAGACAGATCAATGTCCATGTCTTATGAGCGTTTATGAGTCTATCTGTTGGC 540
 Db 481 GCACAGACAGATCAATGTCCATGTCTTATGAGCGTTTATGAGTCTATCTGTTGGC 540
 QY 541 GGTTCGTAGTCAAAAATGATGAGTCCGTGTGAGTCAACCGAGACGCAAAATGATGCGAGTT 600
 541 GGTTCGTAGTCAAAAATGATGAGTCCGTGTGAGTCAACCGAGACGCAAAATGATGCGAGTT 600
 Db 541 GGTTCGTAGTCAAAAATGATGAGTCCGTGTGAGTCAACCGAGACGCAAAATGATGCGAGTT 600
 QY 601 TTTGTTTACAGATCGTGTTCATCAAAAACGGGATCCGCAACCACTGGAAGGAAACACAT 660
 601 TTTGTTTACAGATCGTGTTCATCAAAAACGGGATCCGCAACCACTGGAAGGAAACACAT 660
 Db 601 TTTGTTTACAGATCGTGTTCATCAAAAACGGGATCCGCAACCACTGGAAGGAAACACAT 660
 QY 661 CGAGAGCTGGAGCAGCTTCATACACTCGGAAAAACAATGAAAGGAGCTCGAGAGCGCA 720
 661 CGAGAGCTGGAGCAGCTTCATACACTCGGAAAAACAATGAAAGGAGCTCGAGAGCGCA 720
 Db 661 CGAGAGCTGGAGCAGCTTCATACACTCGGAAAAACAATGAAAGGAGCTCGAGAGCGCA 720
 QY 721 GAGCTGAAAAAGTGGGAGCGCCGAGACAGAAACGAGTGTGAGTGTGAGTGTGAGTGTGAGT 780
 721 GAGCTGAAAAAGTGGGAGCGCCGAGACAGAAACGAGTGTGAGTGTGAGTGTGAGTGTGAGT 780
 Db 721 GAGCTGAAAAAGTGGGAGCGCCGAGACAGAAACGAGTGTGAGTGTGAGTGTGAGTGTGAGT 780
 QY 781 GTAACAGCTGAGGAGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 840
 781 GTAACAGCTGAGGAGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 840
 Db 781 GTAACAGCTGAGGAGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 840
 QY 841 TTGAAGTACGATTCATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
 841 TTGAAGTACGATTCATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
 Db 841 TTGAAGTACGATTCATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
 QY 901 ATCTCATTTTGTGCTGATGATTTCTCATCTTGAACCTGGAAGAGTGGAAAAAGCTAGG 960
 901 ATCTCATTTTGTGCTGATGATTTCTCATCTTGAACCTGGAAGAGTGGAAAAAGCTAGG 960
 Db 901 ATCTCATTTTGTGCTGATGATTTCTCATCTTGAACCTGGAAGAGTGGAAAAAGCTAGG 960
 QY 961 CCACAAATTTAGGCTCTCTGTGCTGATTTAGATTTTCTGCAATTTTTCCTGATTTGCT 1020
 961 CCACAAATTTAGGCTCTCTGTGCTGATTTAGATTTTCTGCAATTTTTCCTGATTTGCT 1020
 Db 961 CCACAAATTTAGGCTCTCTGTGCTGATTTAGATTTTCTGCAATTTTTCCTGATTTGCT 1020
 QY 1021 TTTTGTGGGCAAAACCTTCTGCGGTAATATCAACCTTTCCTGCTGTCTGTGATCAATTC 1080
 1021 TTTTGTGGGCAAAACCTTCTGCGGTAATATCAACCTTTCCTGCTGTCTGTGATCAATTC 1080
 Db 1021 TTTTGTGGGCAAAACCTTCTGCGGTAATATCAACCTTTCCTGCTGTCTGTGATCAATTC 1080
 QY 1081 GTCAAAAACCTTGAACCTTCTGCGGTAATATCAACCTTTCCTGCTGTCTGTGATCAATTC 1140
 1081 GTCAAAAACCTTGAACCTTCTGCGGTAATATCAACCTTTCCTGCTGTCTGTGATCAATTC 1140
 Db 1081 GTCAAAAACCTTGAACCTTCTGCGGTAATATCAACCTTTCCTGCTGTCTGTGATCAATTC 1140
 QY 1141 CATTTTCAAAAGTACCTCTGTATCTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
 1141 CATTTTCAAAAGTACCTCTGTATCTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
 Db 1141 CATTTTCAAAAGTACCTCTGTATCTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
 QY 1201 GTGGGCTCTTCCAACTCCCGCAAAATTCCTGTACGCGTACGAGCTTTGTATTTATTTT 1260
 1201 GTGGGCTCTTCCAACTCCCGCAAAATTCCTGTACGCGTACGAGCTTTGTATTTATTTT 1260
 Db 1201 GTGGGCTCTTCCAACTCCCGCAAAATTCCTGTACGCGTACGAGCTTTGTATTTATTTT 1260
 QY 1261 TTCAAAATTTGTTCTCTCTACAAACAAAAAAGGTTCAAAAAA 1315

Db 1261 TTCAAAATTTGTTCTCTCTACAAACAAAAAAGGTTCAAAAAA 1315
 RESULT 14
 US-07-927-681-1
 ? Sequence 1, Application US/07927681
 ? GENERAL INFORMATION:
 ? APPLICANT: Horvitz, H. Robert
 ? APPLICANT: Hengartner, Michael
 ? TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 ? TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL
 ? TITLE OF INVENTION: DEATH AND USES THEREFOR
 ? NUMBER OF SEQUENCES: 5
 ? CORRESPONDENCE ADDRESSES:
 ? ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 ? STREET: Two Millia Drive
 ? CITY: Lexington
 ? STATE: Massachusetts
 ? COUNTRY: U.S.A.
 ? ZIP: 02173-4799
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/07/927,681
 ? FILING DATE: 10-AUG-1992
 ? CLASSIFICATION: 424
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Granahan, Patricia
 ? REGISTRATION NUMBER: 32,227
 ? REFERENCE/DOCKET NUMBER: MIT-5934A
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (617) 861-6240
 ? TELEFAX: (617) 861-9540
 ? TELEX: 951794
 ? INFORMATION FOR SEQ ID NO: 1:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 6559 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: double
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: DNA (genomic)
 ? US-07-927-681-1
 Query Match 48.1%; Score 632.6; DB 3; Length 6559;
 Best Local Similarity 99.8%; Pred. No. 4.4e-133;
 Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 669 GAGAGACTTCATGACACTCGGAAACAAATGAAAGAGACTACGAAAGGAGGAGGAGTGA 728
 669 GAGAGACTTCATGACACTCGGAAACAAATGAAAGAGAGTACGAAAGGAGGAGGAGTGA 728
 Db 3392 GAGAGACTTCATGACACTCGGAAACAAATGAAAGAGAGTACGAAAGGAGGAGTGA 3451
 QY 729 AAAAGTGGGAGCGCCGAG 788
 729 AAAAGTGGGAGCGCCGAG 788
 Db 3452 AAAAGTGGGAGCGCCGAG 3511
 QY 789 TGGAGCATTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 848
 789 TGGAGCATTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 848
 Db 3512 TGGAGCATTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3571
 QY 849 ACGTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 908
 849 ACGTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 908
 Db 3572 ACGTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3631
 QY 909 TTKGCTACTGATTTCTGCTACTCTTTGAACTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 968
 909 TTKGCTACTGATTTCTGCTACTCTTTGAACTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 968
 Db 3632 TTKGCTACTGATTTCTGCTACTCTTTGAACTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 3691
 QY 969 TAGGCTCTGCTGTGATTTAGATTTTCTCAATTTTTCGATTTGCTTTT 1028
 969 TAGGCTCTGCTGTGATTTAGATTTTCTCAATTTTTCGATTTGCTTTT 1028

GenCore version 5.1.4.P5_4578
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 20:35:45 : Search time 620.847 Seconds
(without alignments)
3609.239 Million cell updates/sec

Title: US-09-993-420a-2

Perfect score: 1315
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3936061 seqs, 852009584 residues

Total number of hits satisfying chosen parameters: 7872122

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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7: /cgn2_6/prodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40.4	3.1	4620	US-10-144-771-6694	Sequence 6694, Ap
2	39.6	3.0	364	US-09-531-113-3558	Sequence 3558, Ap
3	38.4	2.9	8323	US-10-311-455-31	Sequence 31, Appl
4	38.2	2.9	6222	US-10-310-673-2117	Sequence 665, App
5	38	2.9	369	US-10-310-673-2117	Sequence 2117, Ap
6	38	2.9	502	US-09-531-113-6153	Sequence 6153, Ap
7	38	2.9	17848	US-10-240-453-37	Sequence 37, Appl
8	38	2.9	17848	US-10-257-166-57	Sequence 57, Appl
9	37.8	2.9	417	US-09-513-999C-28718	Sequence 28718, A
10	37.4	2.8	6229	US-10-311-455-237	Sequence 237, App
11	37.2	2.8	297	US-10-310-673-1846	Sequence 1846, Ap
12	37.2	2.8	15732	US-10-240-453-108	Sequence 108, Appl
13	37	2.8	180216	US-10-308-485-6	Sequence 6, Appl
14	36.8	2.8	425	US-09-531-113-12891	Sequence 12891, A
15	36.8	2.8	5317	US-10-311-455-581	Sequence 581, App
16	36.6	2.8	1825	US-60-427-313-7	Sequence 7, Appl
17	36.6	2.8	1840	US-10-017-161-3359	Sequence 2359, Ap
18	36.6	2.8	9206	US-10-311-455-1648	Sequence 1648, Ap
19	36.6	2.8	9964	US-10-311-455-71	Sequence 71, Appl
20	36.4	2.8	414	US-09-531-113-3971	Sequence 3971, Appl
21	36.4	2.8	431	US-09-724-676-30591	Sequence 30591, A
22	36.4	2.8	431	US-09-724-676A-30591	Sequence 30591, A
23	36.4	2.8	478	US-09-724-676A-30585	Sequence 30585, A
24	36.4	2.8	478	US-09-724-676A-30585	Sequence 30585, A
25	36.4	2.8	523	US-09-724-676A-30588	Sequence 30588, A
26	36.4	2.8	523	US-09-724-676A-30588	Sequence 30588, A

C 27	36.4	2.8	570	5	US-09-724-676-30583	Sequence 30583, A
C 28	36.4	2.8	570	5	US-09-724-676A-30583	Sequence 30583, A
C 29	36.4	2.8	634	5	US-09-724-676-30587	Sequence 30587, A
C 30	36.4	2.8	634	5	US-09-724-676-30587	Sequence 30587, A
C 31	36.4	2.8	681	5	US-09-724-676-30587	Sequence 30587, A
C 32	36.4	2.8	681	5	US-09-724-676-30587	Sequence 30587, A
C 33	36.4	2.8	681	5	US-09-724-676A-30582	Sequence 30586, A
C 34	36.4	2.8	681	5	US-09-724-676A-30582	Sequence 30586, A
C 35	36.4	2.8	728	5	US-09-724-676A-30586	Sequence 30586, A
C 36	36.4	2.8	728	5	US-09-724-676-30581	Sequence 30581, A
C 37	36.4	2.8	891	5	US-09-724-676A-30581	Sequence 30581, A
C 38	36.4	2.8	891	5	US-09-724-676A-30590	Sequence 30590, A
C 39	36.4	2.8	959	5	US-09-724-676A-30590	Sequence 30590, A
C 40	36.4	2.8	959	5	US-09-724-676A-30579	Sequence 30579, A
C 41	36.4	2.8	983	5	US-09-724-676A-30598	Sequence 30598, A
C 42	36.4	2.8	983	5	US-09-724-676A-30598	Sequence 30598, A
C 43	36.4	2.8	1094	5	US-09-724-676-30597	Sequence 30597, A
C 44	36.4	2.8	1094	5	US-09-724-676A-30597	Sequence 30597, A
C 45	36.4	2.8	1132	5	US-09-724-676-30596	Sequence 30596, A

ALIGNMENTS

RESULT 1
US-10-144-771-6694
Sequence 6694, Application US/10144771
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
FILE REFERENCE: C1001321
CURRENT APPLICATION NUMBER: US/10/144,771
CURRENT FILING DATE: 2002-05-15
NUMBER OF SEQ ID NOS: 47235
SEQ ID NO 6694
LENGTH: 4620
TYPE: DNA
ORGANISM: HUMAN
US-10-144-771-6694

Query Match
Best Local Similarity 48.7%; Pred. No. 1.1;
Matches 110; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1055 CAACCTTCCGCTGCTCTGCTACATTTGCTCAAAACCCGTAACCTTCTGCGC 1114
DB 2983 CAACATACCCCAATATGATTTCTCTTCCCTGCTGCTCCCTTCCCTCCAT 3042
QY 1115 TGGCTACCTCCGCTCTCTTCCACATTTCCAAAGAACCCGTAATCAATATCA 1174
DB 3043 TTCCCTCCCTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3102
QY 1175 TCTTACCTTACGCTCTCTTCTGCTGCTGCTTCCAACTCCCAATTCCTGTAC 1234
DB 3103 CTGCTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3162
QY 1235 GCGTACGCTTGTATTTATTTTTCAAATGTTTCTCTCA 1280
DB 3163 CTGCT 3208

RESULT 2
US-09-531-113-3558/C
Sequence 3558, Application US/09531113
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-21(15761)B
CURRENT APPLICATION NUMBER: US/09/531, 113
CURRENT FILING DATE: 2000-03-22

FEATURE:

b
14312 AACCTCCTTAATAACCAAAACAAGCCATCGTTCGATTGGTTGCTGC

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: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (2183, 8830, 9169, 9333, 9339, 11774)
US-10-240-453-37

Query Match
Best Local Similarity 50.0%; Score 38; DB 6; Length 17848;
Matches 121; Conservative 0; Mismatches 120; Indels 1; Gaps 1

Y 1069 TCTGTACATTTGCTCAAAAACCCCTGAACCCCTAATCTTTTCGCGCGGAGCTAGCCGCC 1128
Db 14372 TTTCAAAATATTCACAAAAAATTCCTAAAAAATATATTTATCTGCTCATTACTTCAA 14313
QY 1129 GCTTCTCTCCACATTTTCCAAAGTACCGCTATCTCAATATATCATTTCACTTTAACT 1188
Db 14312 AAACCTCCCTCAATATACCAAAACGCCCTATCT-ACAAAAAACCATATCTTTCACACA 14254
QY 1189 GTCTCTTTTGGTGCGCCCTCTTCCAACTCCGCCCAATTCCTGACGCGTACGCACTT 1248
Db 14253 ATCTCTTATATATATCATATCTCAAACTTACTACAAATTTATTAATATCCAACTTACTA 14194
QY 1249 GATATATTTTTCCTCAAAATTTGTTTCTCTGCTACACACAAAAAAGCTTCAAAAAA 1308
Db 14193 CATCTTCTCTTTTAAATATATCTCTATACACCAAACTAAATCAATATATAT 14134
QY 1309 AA 1310
Db 14133 AA 14132

RESULT 8
US-10-257-166-57/c
: Sequence 57, Application US/10257166
: GENERAL INFORMATION:
: APPLICANT: OLEK, Alexander
: APPLICANT: PIERPENBROCK, Christian
: APPLICANT: BERLIN, Kurt
: TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation o
: TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
: FILE REFERENCE: 5013.1011
: CURRENT APPLICATION NUMBER: US/10/257,166
: CURRENT FILING DATE: 2002-10-07
: PRIOR APPLICATION NUMBER: PCT/EP01/07470
: DE 10032529.7
: DE 10043826.1
: PRIOR FILING DATE: 2001-06-29
: 2000-06-30
: 2000-09-01
: NUMBER OF SEQ ID NOS: 178
: SEQ ID NO 57
: LENGTH: 17848
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (2183, 8830, 9169, 9333, 9339, 11774)
US-10-257-166-57

Query Match
Best Local Similarity 50.0%; Score 38; DB 6; Length 17848;
Matches 121; Conservative 0; Mismatches 120; Indels 1; Gaps 1,

```

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QY 1189 GTCCTTTTGGTGGCCCTCTTCCAACTCCGCCAAATTCGTACGGGTACGCGACTTT 1248
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 14253 ATCTCTTAATATATCTACTCTCACTCAAACTACTACATTAATTAATCCAACTTAACCTA 14194
QY 1249 GATATTTATTTTTCATATTTGTTTCTCTCTCTACACACAAAAAAGCGTTCAAAAAA 1308
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 14193 CTATCTTCTCTTTAAATAAATATCTCTCTATCACCACCAACTAAATACATTAATAT 14134
QY 1309 AA 1310
      ||
Db 14133 AA 14132

RESULT 9
US-09-513-999C-28718/c
; Sequence 28718, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG.
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 28718
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 348
; OTHER INFORMATION: v=a or c or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 401
; OTHER INFORMATION: w=a or t
US-09-513-999C-28718

Query Match
Best Local Similarity 60.0%; Score 37.8; DB 5; Length 417;
Matches 63; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 669 GGACGACTTCATGACACTCGGAAAAAATGAAAGAGACTACGACGACGAGAGCTGA 728
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 108 GGAATATATTTCTGACACTAGAGATGCAATGAAAGACTGCTGGAGATATGAGAAGCTCC 49
QY 729 AAAAGTGGAGCGCCGGAAGCAGACAGACAGCGGTGTCATGATTTG 773
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 48 TGAAGTAGGCGAGTGTGATAGATGAGTAGAGAGGGGGGATGATGG 4

RESULT 10
US-10-311-455-237/c
; Sequence 237, Application US/10311455
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detect
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01

; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 237
; LENGTH: 6229
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-237

Query Match
Best Local Similarity 58.6%; Score 37.4; DB 6; Length 6229;
Matches 65; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1205 CCTCTCCAACTCCGCCAAATTCCTGTACGCGTACGCGACTTGTATTTATTTTCA 1264
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1162 CCTAAAGTACACATCTATCTACTTCTCTCAATAAACATATTTTATTTATTTAT 1103
QY 1265 AATTGTTTCTCTCTACACAAAAAAGCGTTCAAAAAA 1315
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1102 TTTCTAAATTTTACCAAAAAA 1052

RESULT 11
US-10-310-673-1846
; Sequence 1846, Application US/10310673
; GENERAL INFORMATION:
; APPLICANT: Garcia, Pablo
; APPLICANT: Escobedo, Jaime
; APPLICANT: Lamson, George
; APPLICANT: Randazzo, Filippo
; APPLICANT: Moler, Edward
; APPLICANT: Klinger, Julie
; APPLICANT: Janatpour, Mary Jo
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; TITLE OF INVENTION: IN CANCEROUS PROSTATE CELLS AND THEIR METHODS OF USE
; FILE REFERENCE: 18095.002
; CURRENT APPLICATION NUMBER: US/10/310,673
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/336,613
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 2164
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1846
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-673-1846

Query Match
Best Local Similarity 55.4%; Score 37.2; DB 6; Length 297;
Matches 72; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1132 TCTCTCCAACTTCGAAAGTACCCCTGTATCTCAATTAATCATCTTCACTTAAGTTC 1191
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 66 TCTGTATCTATATCTATTTAAATTCAGCTCAATTCATTCACACCTACTCCAAACTTC 125
QY 1192 TCTTTTGGTGGCTCTTCAACTCCGCCAAATTCGTACGCGACTTGTGA 1251
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 126 TCTTTCCAGCTACTTACTCTCTCTCTCAATTCACACTTCTCTGCTACTTTT 185
QY 1252 TTTATTTT 1261
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 186 TTTT 195

RESULT 12
US-10-240-453-108/c
; Sequence 108, Application US/10240453
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
```

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; TITLE OF INVENTION: Transcription
; TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
; FILE REFERENCE: 5013.1009
; CURRENT APPLICATION NUMBER: US/10/240,453
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03973
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 108
; LENGTH: 15732
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-240-453-108
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Query Match
Best Local Similarity 2.8%; Score 37.2; DB 6; Length 15732;
Matches 114; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
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QY 867 AATAATTAATTAATGATGACCTGCTTACATTTGATTCATTTGGCTGATTTCTCT 926
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8134 AATAATTCCTTTTACGATCCTCCACACACACTAATTTCTAATAATTTATTTT 8075
QY 927 CATCCTTGAACGAGAGAGTGGAAGCTAGCCACAAATTCAGGCTCTGTGCGA 986
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8074 AACAAATACCAAAACATCATCTTAACAACTCCGATTTATATACATATATTTTAA 8015
QY 987 TTACGATTTTTCGCAATTTTTCGCCATTTTTCGCTTTTTCGCTTTTTCGCT 1046
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8014 TATTTATCTCTTTATTAATTTTATTAATTTTATTAATTTTCTAATAATTTTAC 7955
QY 1047 GCTAATATCACTTTCCGCTGCTGATTTTCGTCATAAAACCCGTAACCTT 1106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 7954 TTAACATATCATATATATTAATTAACCATTTATATACCTTTTAAAAAATCTAT 7895
QY 1107 TC 1108
    ||
DB 7894 TC 7893
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RESULT 13
US-10-308-485-6
; Sequence 6, Application US/10308485
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/10/308,485
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/835,232
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 180216
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (1)...(180216)
; OTHER INFORMATION: n = A,T,C or G
US-10-308-485-6
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Query Match
Best Local Similarity 2.8%; Score 37; DB 6; Length 180216;
Matches 67; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
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QY 664 AGCTGGGACGACTTCATGACACTCGGAAAAAATGAAAGAGACTACGACGACGAA 723
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 19646 AGCTGGGACGACGAGAGTCTCCAAAACAAACAAACAAACAAACAAACAAAC 19705
QY 724 GCTGAAAAAATGGAGCCGGAAGACAGAACAGCGGTGCTGATGTTGGCGCTGA 780
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DB 19706 AAAACACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 19762
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RESULT 14
US-09-531-113-12891
; Sequence 12891, Application US/09531113
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15761)B
; CURRENT APPLICATION NUMBER: US/09/531,113
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 48629
; SEQ ID NO 12891
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: jC-gmfl02220143a08d1
US-09-531-113-12891
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Query Match
Best Local Similarity 2.8%; Score 36.8; DB 5; Length 425;
Matches 50; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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QY 1244 ACTTGATTAATTTTTCATTAATTTTCTCTCTACACAAACAAACGTTCAA 1303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 72 ATTTTATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 131
QY 1304 AAAAAAAAAA 1315
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DB 132 AAAAAAAAAA 143
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RESULT 15
US-10-311-455-581/C
; Sequence 581, Application US/10311455
; GENERAL INFORMATION:
; APPLICANT: Olek, Alexander
; APPLICANT: Piepenbrock, Christian
; APPLICANT: Berlin, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Det
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 581
; LENGTH: 5317
; TYPE: DNA
; ORGANISM: Artificial Sequence
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GenCore version 5.1.4.P5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 18:42:50 ; Search time 1592.53 Seconds

(without alignments)
13373.121 Million cell updates/sec

Title: US-09-993-420A-2

Perfect score: 1315

Sequence: 1 ttgagatgacacgctgcac.....cgttcaaaaaaaaaaaaaa 1315

Scoring table: IDENTITY_NTC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	372	28.3	372	9	AV186746
2	360	27.4	360	14	AV186746
3	355	27.0	375	14	C39347
4	314.6	23.9	323	14	D73048
5	299	22.7	300	9	AV181369
6	295.6	22.5	360	9	AV191206

C 7	279.6	21.3	300	14	C39078	C39078	C39078	Yuj1
C 8	275.6	21.0	300	14	C31912	C31912	C31912	Yuj1
C 9	269.2	20.5	300	14	C29364	C29364	C29364	Yuj1
C 10	261	19.8	360	9	AV193616	AV193616	AV193616	Yuj1
C 11	259.4	19.7	300	9	AV179317	AV179317	AV179317	Yuj1
C 12	68.4	5.2	1101	17	CNS0106X	CNS0106X	CNS0106X	Yuj1
C 13	65.8	5.0	1101	17	CNS0039G	CNS0039G	CNS0039G	Yuj1
C 14	65.2	5.0	997	17	CNS005TE	CNS005TE	CNS005TE	Yuj1
C 15	56.6	4.3	1101	17	CNS0182P	CNS0182P	CNS0182P	Yuj1
C 16	53.2	4.0	1101	17	CNS0039G	CNS0039G	CNS0039G	Yuj1
C 17	52.4	4.0	1101	17	CNS0181N	CNS0181N	CNS0181N	Yuj1
C 18	50.4	3.8	987	17	CNS00418	CNS00418	CNS00418	Yuj1
C 19	50.4	3.8	1201	17	CNS016DO	CNS016DO	CNS016DO	Yuj1
C 20	49.6	3.7	1201	17	CNS00418	CNS00418	CNS00418	Yuj1
C 21	48.8	3.7	1201	17	CNS01660	CNS01660	CNS01660	Yuj1
C 22	48.6	3.7	808	10	BE033818	BE033818	BE033818	Yuj1
C 23	48	3.7	1201	17	CNS016DW	CNS016DW	CNS016DW	Yuj1
C 24	47.8	3.6	925	17	CNS00DSE	CNS00DSE	CNS00DSE	Yuj1
C 25	47.6	3.6	801	17	AG045123	AG045123	AG045123	Yuj1
C 26	47.6	3.6	850	12	BE966968	BE966968	BE966968	Yuj1
C 27	47.4	3.6	762	9	AL514493	AL514493	AL514493	Yuj1
C 28	47.2	3.6	908	17	CNS01678	CNS01678	CNS01678	Yuj1
C 29	47.2	3.6	1204	17	CNS016E2	CNS016E2	CNS016E2	Yuj1
C 30	45.8	3.5	411	9	AL1635287	AL1635287	AL1635287	Yuj1
C 31	45.8	3.5	914	17	BH152037	BH152037	BH152037	Yuj1
C 32	45.8	3.5	935	17	CNS010G4	CNS010G4	CNS010G4	Yuj1
C 33	45.8	3.5	1183	17	CNS016CR	CNS016CR	CNS016CR	Yuj1
C 34	45.2	3.4	1201	17	CNS01613	CNS01613	CNS01613	Yuj1
C 35	45	3.4	421	10	AM460090	AM460090	AM460090	Yuj1
C 36	45	3.4	583	9	CNS0440G	CNS0440G	CNS0440G	Yuj1
C 37	45	3.4	633	9	AL513979	AL513979	AL513979	Yuj1
C 38	44.8	3.4	394	9	AL1491775	AL1491775	AL1491775	Yuj1
C 39	44.8	3.4	920	17	AZ691914	AZ691914	AZ691914	Yuj1
C 40	44.8	3.4	1101	17	CNS016RG	CNS016RG	CNS016RG	Yuj1
C 41	44.6	3.4	450	9	AL513867	AL513867	AL513867	Yuj1
C 42	44.6	3.4	527	9	AL514325	AL514325	AL514325	Yuj1
C 43	44.6	3.4	1179	17	CNS001CW	CNS001CW	CNS001CW	Yuj1
C 44	44.4	3.4	882	17	CNS00CEK	CNS00CEK	CNS00CEK	Yuj1
C 45	44.2	3.4	504	14	B0524016	B0524016	B0524016	Yuj1

ALIGNMENTS

RESULT 1
AV186746
LOCUS
DEFINITION
AV186746 yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans CDNA clone yk503f3 5', mRNA sequence.
ACCESSION
AV186746
VERSION
AV186746.1 GI:5568729
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans.
ORGANISM
Caenorhabditis elegans.
REFERENCE
1 (bases 1 to 372)
Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H., Nishigaki, A., Morinashi, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and Nomoto, H.
Expressed genes in C.elegans
Unpublished (1999)
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1..372
/organism="Caenorhabditis elegans"

TITLE
JOURNAL
COMMENT

FEATURES
source

/strain="N2"
/db_xref="taxon:6239"
/clone="yk503f3"
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hermaphrodite embryo"
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/dev_stage="embryo"
BASE COUNT 105 a 75 c 118 g 74 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.2e-68;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGAGATGACAGCGTTCGACGCGGACCACTCGTACGATCCGCGTATCGGCGAGAA 61
DB 1 TTGAGATGACAGCGTTCGACGCGGACCACTCGTACGATCCGCGTATCGGCGAGAA 60
QY 62 CGATGGCGACTGGCGAGATGAAGAGATTCTGCGGATTAAGGACACAGCCCGAGATT 121
DB 61 CGATGGCGACTGGCGAGATGAAGAGATTCTGCGGATTAAGGACACAGCCCGAGATT 120
QY 122 TTGGAATCAATAGTGTGCTCAGGACTTGCATACCGAGTAAAGGCGCTTGCAGCGAA 181
DB 121 TTGGAATCAATAGTGTGCTCAGGACTTGCATACCGAGTAAAGGCGCTTGCAGCGAA 180
QY 182 GAATGTCATCGAGAGATCAATTGATGAAAAATCAATGATGGAGAGCCAGGCTTG 241
DB 181 GAATGTCATCGAGAGATCAATTGATGAAAAATCAATGATGGAGAGCCAGGCTTG 240
QY 242 ATATCGAGGATTTGTGCTGATATTTCCGACCGAATCCGGCAAAACGGAATGAAAT 301
DB 241 ATATCGAGGATTTGTGCTGATATTTCCGACCGAATCCGGCAAAACGGAATGAAAT 300
QY 302 GATTGGAGACCGGAGATTCCTGTGAGTGCACCGGAGACGAGAAATGATGCGAGTTA 361
DB 301 GATTGGAGACCGGAGATTCCTGTGAGTGCACCGGAGACGAGAAATGATGCGAGTTA 360
QY 362 TGGAGACGATAT 373
DB 361 TGGAGACGATAT 372

RESULT 2
C39347 360 bp mRNA linear EST 18-OCT-1999
LOCUS C39347 Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo
DEFINITION Caenorhabditis elegans cDNA clone yk201b10 5', mRNA sequence.
ACCESSION C39347
VERSION C39347.1 GI:2375584
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yui Kohara
National Institute of Genetics
Genome Biology Lab.
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
location/Qualifiers
FEATURES
source 1..360
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
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/clone_lib="Yui Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT 106 a 69 c 114 g 71 t
ORIGIN

Query Match 27.4%; Score 360; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.7e-65;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGATCCGCGGATTCGCGGACGAGATGCGGACTGGCGGATGAAGGAGATTCTGCGGGA 97
DB 1 CGATCCGCGGATTCGCGGACGAGATGCGGACTGGCGGATGAAGGAGATTCTGCGGGA 60
QY 98 TAAAGGACAGAGCCCGGACGATTTTGAATCAATATGATGCTCAGGACTTGCATCAC 157
DB 61 TAAAGGACAGAGCCCGGACGATTTTGAATCAATATGATGCTCAGGACTTGCATCAC 120
QY 158 CGATGAGCAGGCTTCGACGCGGAGAAATGTCATCGAGATCAATTGATGAAAAATCA 217
DB 121 CGATGAGCAGGCTTCGACGCGGAGAAATGTCATCGAGATCAATTGATGAAAAATCA 180
QY 218 ATGATGGGAAAGACCAAGGCTTATATGAGGAGATTTGTGCTGATATTTCCAGCACC 277
DB 181 ATGATGGGAAAGACCAAGGCTTATATGAGGAGATTTGTGCTGATATTTCCAGCACC 240
QY 278 GAATCCGCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 337
DB 241 GAATCCGCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
QY 338 CGGACGACGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 397
DB 301 CGGACGACGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360

RESULT 3
C42506 375 bp mRNA linear EST 18-OCT-1999
LOCUS C42506 Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo
DEFINITION Caenorhabditis elegans cDNA clone yk312c5 5', mRNA sequence.
ACCESSION C42506
VERSION C42506.1 GI:2378743
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE 1 (bases 1 to 375)
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yui Kohara
National Institute of Genetics
Genome Biology Lab.
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
location/Qualifiers
FEATURES
source 1..375
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk312c5"
/clone_lib="Yui Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"

BASE COUNT 107 a 77 c 118 g 72 t 1 others
ORIGIN

Query Match 27.0%; Score 355; DB 14; Length 375;
 Best Local Similarity 99.7%; Pred. No. 1,9e-64;
 Matches 366; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 10 ACACCTTCACGGGAGGACACTGCTGACGAATCCGGGATTCGGGACAGAACGATGGCG 69
 Db 1 ACACCTTCACGGGAGGAGCACTGCTGACGAATCCGGGATTCGGGACAGAACGATGGCG 60
 QY 70 ACTGGCGAGTGAAGGAGATTCT-GGGGATTAAGGACAGAGCCGCCGATTTTGAAT 128
 Db 61 ACTGGCGAGTGAAGGAGATTCTGCGGATTAAGGACAGAGCCGCCGATTTTGAAT 120
 QY 129 CAATAGTGAAGTCAAGGATTCGACGAGTGAAGGACAGGATTTGATTCGA 248
 Db 121 CAATAGTGAAGTCAAGGATTCGACGAGTGAAGGACAGGATTTGATTCGA 180
 QY 189 CATGGAGAGTCAATGATGAAAAATCAATGATGGGAGAGCCGATTTGATTCGA 248
 Db 181 CATGGAGAGTCAATGATGAAAAATCAATGATGGGAGAGCCGATTTGATTCGA 240
 QY 249 GGGATTTGTGCTGACTATTTTCACGACGATCCGGCAAGGAAATGGAATGCTTGG 308
 Db 241 GGGATTTGTGCTGACTATTTTCACGACGATCCGGCAAGGAAATGGAATGCTTGG 300
 QY 309 AGACCGGGATTCGCTGCTGAGTGAACCGGACAGCAAGAAATGATGATTTGGAAC 368
 Db 301 AGACCGGGATTCGCTGCTGAGTGAACCGGACAGCAAGAAATGATGATTTGGAAC 360
 QY 369 GATATTC 375
 Db 361 GATATTC 367

RESULT 4
 LOCUS D73048/c 323 bp mRNA linear EST 18-OCT-1999
 DEFINITION CELK113B7R Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
 embryo Caenorhabditis elegans cDNA clone yk113b7 3', mRNA sequence.
 ACCESSION D73048
 VERSION D73048.1 GI:1112756
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabdilitoidea
 ; Rhabdilitidae; Peloderiinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 323)
 AUTHORS Kohara,Y., Mitsuiki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
 Tabara,H.
 TITLE Toward an expression map of the C.elegans genome
 JOURNAL Unpublished (1994)
 COMMENT Contact: Yuji Kohara
 Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: yk@kharalab.nig.ac.jp.
 FEATURES
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 /organism="Caenorhabditis elegans"
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 hermaphrodite embryo"
 /sex="hermaphrodite"
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BASE COUNT 118 a 40 c 67 t 2 others
 ORIGIN

Query Match 23.9%; Score 314.6; DB 14; Length 323;
 Best Local Similarity 98.1%; Pred. No. 6.1e-56;
 Matches 317; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 956 CTAGGCCACAATAATTAGGCTCTGCTGATTTAGATTTTACTGCATTTTTCAGAT 1015
 Db 323 CTAGGCCACAATAATTAGGCTCTGCTGATTTAGATTTTACTGCATTTTTCAGAT 264
 QY 1016 TGCCTTTTTTTTTGGCCAAACCTTACTCCGGGATATATCACTTTCCGTGCTGAC 1075
 Db 263 TGCCTTTTTTTTTGGCCAAACCTTACTCCGGGATATATCACTTTCCGTGCTGAC 204
 QY 1076 ATTTCGTCAAAAACCTTAAACCTTAACTTTCTGCGGCTGACCTCCGCTCTC 1135
 Db 203 ATTTCGTCAAAAACCTTAAACCTTAACTTTCTGCGGCTGACCTCCGCTCTC 144
 QY 1136 TTCCACATTTCCAAAGTACCCCTGATCTCATATATCATCTTCACTTACTGCTCTT 1195
 Db 143 TTCCACATTTCCAAAGTACCCCTGATCTCATATATCATCTTCACTTACTGCTCTT 84
 QY 1196 TTGCTGTGGCTCTTCCAACTCCGCCAAATTCCTGACGGGTACGCACTTTGATTTA 1255
 Db 83 TTGCTGTGGCTCTTCCAACTCCGCCAAATTCCTGACGGGTACGCACTTTGATTTA 24
 QY 1256 TTTTTCATTTGTTTCTCTC 1278
 Db 23 TTTTTCATTTGTTTCTCTC 1

RESULT 5
 LOCUS AV181369/c 300 bp mRNA linear EST 21-JUL-1999
 DEFINITION AV181369 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
 embryo Caenorhabditis elegans cDNA clone yk619e10 3', mRNA
 sequence.
 ACCESSION AV181369
 VERSION AV181369.1 GI:5561270
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabdilitoidea
 ; Rhabdilitidae; Peloderiinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 300)
 AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuiki,H.,
 Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano
 M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
 Nomoto,H.
 TITLE Expressed genes in C.elegans
 JOURNAL Unpublished (1999)
 COMMENT Contact: Yuji Kohara
 Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: yk@kharalab.nig.ac.jp.
 FEATURES
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BASE COUNT 103 a 44 c 90 g 62 t 1 others
 ORIGIN

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 Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 944 GAAGTGGGAAAGCTAGGACCAAAATTTAGCGCTCTGCTGATTTAGCATTTTACTGCA 1003
 Db 300 GAAGTGGGAAAGCTAGGACCAAAATTTAGCGCTCTGCTGATTTAGCATTTTACTGCA 241

QY 1004 ATTTTTCGGATGCTTTTTCGGCAACCTACTCCGCTAATATCACTTTC 1063
 DB 240 ATTTTTCGGATGCTTTTTCGGCAACCTACTCCGCTAATATCACTTTC 181
 QY 1064 CGTGTCTGTACATTTTCGCAAAACCCGAAACCTAATTTTCGCGGTGAGC 1123
 DB 180 CGGTGTCTGTACATTTTCGCAAAACCCGAAACCTAATTTTCGCGGTGAGC 121
 QY 1124 CTCGCCCTCTCTTCACATTTCCAAAGTACCCCTGTATCTCAATATCTTCACTT 1183
 DB 120 CTCGCCCTCTCTTCACATTTCCAAAGTACCCCTGTATCTCAATATCTTCACTT 61
 QY 1184 TAACTGTCTTTTCTGTGTGGGCTCTTCCACTCCCCCAATTCCTAGCGTACGCG 1243
 DB 60 TAACTGTCTTTTCTGTGTGGGCTCTTCCACTCCCCCAATTCCTGTACGCGTACGCG 1
 RESULT 6
 LOCUS AV191206 360 bp mRNA linear EST 22-JUL-1999
 DEFINITION AV191206 Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo *Caenorhabditis elegans* cDNA clone yk591c12 5', mRNA sequence.
 ACCESSION AV191206.1 GI:5573358
 VERSION AV191206
 KEYWORDS EST.
 SOURCE *Caenorhabditis elegans*.
 ORGANISM *Caenorhabditis elegans*.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabdilitoidea
 ; Rhabdilitidae; Peloderinae; *Caenorhabditis*.
 REFERENCE 1 (bases 1 to 360)
 AUTHORS Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuiki,H., Nishigaki,A., Motobashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitani,Y., Iida,K., Oesugi,H., Sugiyama,Y. and Nomoto,H.
 TITLE Expressed genes in *C. elegans*
 JOURNAL Unpublished (1999)
 COMMENT Contact: Yui Kohara
 Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykohara@lab.nig.ac.jp.
 FEATURES
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 /strain="N2"
 /db_xref="taxon:6239"
 /clone="yk591c12"
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 /sex="hermaphrodite"
 /dev_stage="embryo"
 BASE COUNT 110 a 77 c 93 g 74 t 6 others
 ORIGIN
 Query Match 22.5% Score 295.6; DB 9; Length 360;
 Best Local Similarity 90.0% Pred. No. 5.6e-52;
 Matches 324; Conservative 0; Mismatches 35; Indels 1; Gaps 1;
 QY 45 GCGGATCGGCGGCAAGATGGGAGATGGAAGAGTTTCTGGGGATTAAGG 104
 DB 1 GCGGATCGGCGGCAAGATGGGAGATGGAAGAGTTTCTGGGGATTAAGG 60
 QY 105 CACAGAGCCACCGATTTTGAATCAATAGTATGCTCAGACTTTCATCAGCAGTAG 164
 DB 61 CACAGAGCCACCGATTTTGAATCAATAGTATGCTCAGACTTTCATCAGCAGTAG 120
 QY 165 GAGAGCTTGAAGCAAGATGTCATCGAGAGTCAATGTGGAAGAAATCAATGATG 224
 DB 121 GAGAGCTTGAAGCAAGATGTCATCGAGAGTCAATGTGGAAGAAATCAATGATG 180

QY 225 GGAAGACCAAGGCTTGATATCGAGGATTTGTGCTGACTATTTCACGACCGAATCCG 284
 DB 181 GGAAGACCAAGGCTTGATATCGAGGATTTGTGCTGACTATTTCACGACCGAATCCG 240
 QY 285 GCAAAACGGAATGGAATGTTTGAGACCGGGATTTGCGGTGAGTACGACCGAGCA 344
 DB 241 GCAAAACGGAATGGAATGTTTGAGACCGGGATTTGCGGTGAGTACGACCGAGCA 299
 QY 345 CGAATGATCGAGTATGGAACGATATTTGAGAAAGACGACGGAATTTTGAAGC 404
 DB 300 CGAATGATCGAGTATGGAACGATATTTGAGAAAGACGACGGAATTTTGAAGC 359
 RESULT 7
 LOCUS C39078/c 300 bp mRNA linear EST 18-OCT-1999
 DEFINITION C39078 Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo *Caenorhabditis elegans* cDNA clone yk503f3 3', mRNA sequence.
 ACCESSION C39078.1 GI:2375315
 VERSION C39078
 KEYWORDS EST.
 SOURCE *Caenorhabditis elegans*.
 ORGANISM *Caenorhabditis elegans*.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabdilitoidea
 ; Rhabdilitidae; Peloderinae; *Caenorhabditis*.
 REFERENCE 1 (bases 1 to 300)
 AUTHORS Kohara,Y., Motobashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A. and Nishigaki,A.
 TITLE Expression map of the *C. elegans* genome
 JOURNAL Unpublished (1996)
 COMMENT Contact: Yui Kohara
 Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykohara@lab.nig.ac.jp.
 FEATURES
 source
 1..300
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 BASE COUNT 111 a 43 c 68 g 64 t 14 others
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 Best Local Similarity 94.0% Pred. No. 1.4e-48;
 Matches 282; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 QY 918 TGAATCTTCATCCTTTGAACTGGAAGAGTGGAAAGCTAGGCCAACAATAGGCTCT 977
 DB 300 TGAATCTTCATCCTTTGAACTGGAAGAGTGGAAAGTAGGCCAACAATAGGCTCT 241
 QY 978 CTGTGTGATTTACGATTTTACTGCAATTTTTCGATGCTTTTTCGGCAAAAC 1037
 DB 240 TTGTGTGATTTACGATTTTANTGCAATTTTTCGATGCTTTTTCGGCAAAAC 181
 QY 1038 CTACTTCGCGGTATATCAACTTTTCGCGGTCTGTACATTTTCGCAAAACCTGAAAC 1097
 DB 180 NTACTTCGCGGTATATCAANNTTTCGCGGTCTGTACATTTTCGCAAAACCTGAAAC 121
 QY 1098 CTTAATCTTTCTGCGGTGAGCTAGCTCCGCTCTCTTCCACATTTTCCAAAGTACCC 1157
 DB 120 CTTAATCTTTTCGCGGTGAGCTAGCTCCGCTCTCTTCCACATTTTCCAAAGTACCC 61
 QY 1158 TGTATCTCAATTAATCTTCACTTAACTGTCCTTTTCGTCGTGCGCTTCGAAGC 1217
 DB 1158 TGTATCTCAATTAATCTTCACTTAACTGTCCTTTTCGTCGTGCGCTTCGAAGC 1217

Db 60 TGTATCTCAATTAATTCATTACCTTTACTGTCTTTTNGTGGCCCTCTCCACTC 1

RESULT 8
C31912/c 300 bp mRNA linear EST 18-OCT-1999
LOCUS C31912 yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo
DEFINITION C31912 yuji Kohara unpublished cDNA clone yk312c5 3', mRNA sequence.
ACCESSION C31912
VERSION C31912.1 GI:2363708
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae
; Rhabditidae; Peloderae; Caenorhabditis.
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A. and Nishigaki,A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykoha@lab.nig.ac.jp.

FEATURES
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BASE COUNT 105 a 44 c 80 g 64 t 7 others

ORIGIN

Query Match 21.0%; Score 275.6; DB 14; Length 300;
Best Local Similarity 96.0%; Pred. No. 9.7e-48;
Matches 289; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 942 AAGAAGTGGGAAGCTAGGCCACCAATTTACGCTCTGTGCGATTTCAGATTACTG 1001
|||
Db 300 AAGAAGTGGGAAG-TAGGCCACCAATTTACGCGTTTGTGNGATTNANGATTACTG 242
QY 1002 CAATTTTTCGATTCGCTTTTGTGCGCAACCCCTGCGGCTATTCATCACTTT 1061
|||
Db 241 CAATTTTTCGATTCGCTTTTGTGCGCAACCCCTGCGGCTATTCATCACTTT 182
QY 1062 TCCGCTTGTGATTCATTCGCAAAACCCTGAACCCCTGATTTTCGCGGCTA 1121
|||
Db 181 TCCGCTTGTGATTCATTCGCAAAACCCTGAACCCCTGATTTTCGCGGCTA 122
QY 1122 GCGTCCCGCTTGTGATTCATTCGCAAAAGTACCCCTGATTCATCAATTCATCTTAC 1181
|||
Db 121 GCGTCCCGCTTGTGATTCATTCGCAAAAGTACCCCTGATTCATCAATTCATCTTAC 62
QY 1182 TTTAACTGTCTCTTTGCTGTGGCTCTTCAACACCTCCCAAAATTCCTGACGGCTAG 1241
|||
Db 61 TTTAACTGTCTCTTTGCTGTGGCTCTTCAACACCTCCCAAAATTCCTGACGGCTAG 2
QY 1242 C 1242
Db 1 C 1

RESULT 9
C29364/c 300 bp mRNA linear EST 18-OCT-1999
LOCUS C29364 yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo
DEFINITION C29364 yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo

ACCESSION
C29364
C29364.1 GI:261160
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Caenorhabditis elegans cDNA clone yk201b10 3', mRNA sequence.
EST.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae
; Rhabditidae; Peloderae; Caenorhabditis.
Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1996)
Contact: Yuji Kohara
Genome Biology Lab.
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Yata 111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykoha@lab.nig.ac.jp.

FEATURES
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BASE COUNT 105 a 44 c 74 g 63 t 14 others

ORIGIN

Query Match 20.5%; Score 269.2; DB 14; Length 300;
Best Local Similarity 94.0%; Pred. No. 2.1e-46;
Matches 282; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 940 GGAAGAGTGGGAAGCTAGGCCACCAATTTACGCTCTGTGCGATTTCAGATTACTG 999
|||
Db 300 GGAAGAGTGGGAAGGAGTGGGCCACCAATTTACGCTCTGTGNGATTNANGATTACTG 241
QY 1000 TGCATTTTTCGATTCGCTTTTGTGCGCAACCCCTGCGGCTATTCATCACTTT 1059
|||
Db 240 TGCATTTTTCGATTCGCTTTTGTGCGCAACCCCTGCGGCTATTCATCACTTT 181
QY 1060 TTTCCGCTTGTGATTCATTCGCAAAACCCTGAACCCCTGATTTTCGCGGCTAG 1118
|||
Db 180 TTTCCGCTTGTGATTCATTCGCAAAACCCTGAACCCCTGATTTTCGCGGCTAG 121
QY 1119 CTAGCTCCCGCTCTGTGCGATTCGCAAAAGTACCCCTGATTCATCAATTCATCTT 1178
|||
Db 120 CTAGCTCCCGCTCTGTGCGATTCGCAAAAGTACCCCTGATTCATCAATTCATCTT 61
QY 1179 CACTTAACTGTCTCTTTGCTGTGGCTCTTCAACCTCCCAAAATTCCTGACGGCT 1238
|||
Db 60 CACTTAACTGTCTCTTTGCTGTGGCTCTTCAACCTCCCAAAATTCCTGACGGCT 1
RESULT 10
AV193616
AV193616/c 360 bp mRNA linear EST 22-JUL-1999
LOCUS AV193616 yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
DEFINITION AV193616 yuji Kohara unpublished cDNA clone yk619e10 5', mRNA
sequence.
ACCESSION
AV193616
AV193616.1 GI:5575768
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae
; Rhabditidae; Peloderae; Caenorhabditis.
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,

TITLE	Author
Expressed genes in <i>C. elegans</i>	Nomoto, H.

<http://www.egdp.ebi.ac.uk/>. This *Drosophila melanogaster* BAC library (Dros BAC) was used by Alain Billard at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector

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